GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 252.191 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-6
Perfect score: 623
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SGSYFYFDLWGRGTLVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	623	100.0	117	8	ADS87913	Ads87913 Anti-IFN-
2	623	100.0	117	8	ADS94910	Ads94910 Anti-IFN-
3	623	100.0	447	8	ADS87924	Ads87924 Anti-IFN-
4	623	100.0	447	8	ADS94921	Ads94921 Anti-IFN-
5	618	99.2	117	8	ADS87921	Ads87921 Anti-IFN-
6	618	99.2	117	8	ADS94918	Ads94918 Anti-IFN-
7	612	98.2	447	8	ADS87928	Ads87928 Anti-IFN-
8	612	98.2	447	8	ADS94925	Ads94925 Anti-IFN-
9	607	97.4	117	8	ADS87917	Ads87917 Anti-IFN-
10	607	97.4	117	8	ADS94914	Ads94914 Anti-IFN-
11	607	97.4	447	8	ADS87926	Ads87926 Anti-IFN-
12	607	97.4	447	8	ADS94923	Ads94923 Anti-IFN-
13	593	95.2	117	8	ADS87937	Ads87937 Anti-IFN-
14	593	95.2	117	8	ADS94934	Ads94934 Anti-IFN-
15	593	95.2	447	8	ADS87939	Ads87939 Anti-IFN-
16	593	95.2	447	8	ADS94936	Ads94936 Anti-IFN-
17	572	91.8	119	7	ADD69207	Add69207 Human ant
18	566	90.9	118	8	ADP47230	Adp47230 Human pho
19	565	90.7	118	8	ADP47219	Adp47219 Human pho
20	565	90.7	225	6	ABR01525	Abr01525 Human ant
21	564.5	90.6	126	7	ADK18889	Adk18889 Anti-huma
22	563.5	90.4	126	7	ADK18603	Adk18603 Anti-huma
23	563.5	90.4	126	7	ADK18790	Adk18790 Anti-huma
24	563.5	90.4	126	7	ADK18825	Adk18825 Anti-huma
25	563.5	90.4	126	8	ADL25424	Adl25424 Human mAb
26	562	90.2	118	8	ADP47220	Adp47220 Human pho
27	562	90.2	266	8	ADF69305	Adf69305 Human lun
28	560.5	90.0	226	6	ABR01542	Abr01542 Human ant
29	559.5	89.8	126	7	ADK18827	Adk18827 Anti-huma
30	559.5	89.8	126	7	ADK18611	Adk18611 Anti-huma
31	559.5	89.8	126	7	ADK18792	Adk18792 Anti-huma
32	559.5	89.8	126	7	ADK18913	Adk18913 Anti-huma
33	559.5	89.8	126	8	ADL25440	Adl25440 Human mAb
34	559	89.7	118	8	ADP47228	Adp47228 Human pho
35	559	89.7	245	4	AAB67621	Aab67621 Human leu
36	559	89.7	245	4	AAB67622	Aab67622 Human leu
37	558.5	89.6	224	6	ABR01533	Abr01533 Human ant
38	557.5	89.5	126	7	ADK18876	Adk18876 Anti-huma
39	557.5	89.5	126	7	ADK18599	Adk18599 Anti-huma
40	557.5	89.5	126	7	ADK18824	Adk18824 Anti-huma
41	557.5	89.5	126	8	ADL25416	Adl25416 Human mAb
42	557.5	89.5	224	6	ABR01544	Abr01544 Human ant
43	557	89.4	225	6	ABR01529	Abr01529 Human ant
44	556	89.2	118	8	ADP47115	Adp47115 Human pho
45	556	89.2	118	8	ADP47226	Adp47226 Human pho

ALIGNMENTS

RESULT 1
ADS87913
ID ADS87913 standard; protein; 117 AA.
XX
AC ADS87913;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:6.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87912.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 6; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising

CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 623; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
Db 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117

RESULT 2
ADS94910
ID ADS94910 standard; protein; 117 AA.
XX
AC ADS94910;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:6.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94909.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 6; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 623; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
Db 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117

RESULT 3
ADS87924
ID ADS87924 standard; protein; 447 AA.
XX
AC ADS87924;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX

PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 17; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 623; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
Db 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117

RESULT 4
ADS94921
ID ADS94921 standard; protein; 447 AA.
XX
AC ADS94921;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 17; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 623; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
Db 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117

RESULT 5
ADS87921
ID ADS87921 standard; protein; 117 AA.
XX
AC ADS87921;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:14.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX

OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87920.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 99.2%; Score 618; DB 8; Length 117;
Best Local Similarity 99.1%; Pred. No. 7.1e-50;
Matches 116; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117
```

RESULT 6
ADS94918
ID ADS94918 standard; protein; 117 AA.
XX
AC ADS94918;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:14.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94917.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 99.2%; Score 618; DB 8; Length 117;
Best Local Similarity 99.1%; Pred. No. 7.1e-50;
Matches 116; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117
```

RESULT 7
ADS87928
ID ADS87928 standard; protein; 447 AA.
XX
AC ADS87928;

```
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 12; SEQ ID NO 21; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             98.2%;  Score 612;  DB 8;  Length 447;
  Best Local Similarity   98.3%;  Pred. No. 1e-48;
  Matches  115;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117

RESULT 8
ADS94925
ID   ADS94925 standard; protein; 447 AA.
XX
AC   ADS94925;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 14; SEQ ID NO 21; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             98.2%;  Score 612;  DB 8;  Length 447;
  Best Local Similarity   98.3%;  Pred. No. 1e-48;
  Matches  115;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117


RESULT 9
ADS87917
ID   ADS87917 standard; protein; 117 AA.
XX
AC   ADS87917;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:10.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
DR   N-PSDB; ADS87916.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 6; SEQ ID NO 10; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 117 AA;

  Query Match             97.4%;  Score 607;  DB 8;  Length 117;
  Best Local Similarity   97.4%;  Pred. No. 7.5e-49;
  Matches  114;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117


RESULT 10
ADS94914
ID   ADS94914 standard; protein; 117 AA.
XX
AC   ADS94914;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:10.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
DR   N-PSDB; ADS94913.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 8; SEQ ID NO 10; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
```

CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 97.4%; Score 607; DB 8; Length 117;
Best Local Similarity 97.4%; Pred. No. 7.5e-49;
Matches 114; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117
```

RESULT 11
ADS87926
ID ADS87926 standard; protein; 447 AA.
XX
AC ADS87926;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 19; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 97.4%; Score 607; DB 8; Length 447;
Best Local Similarity 97.4%; Pred. No. 3.1e-48;
Matches 114; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117
```

RESULT 12
ADS94923
ID ADS94923 standard; protein; 447 AA.
XX
AC ADS94923;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 heavy chain SEQ ID NO:19.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 19; 115pp; English.

```
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match             97.4%;  Score 607;  DB 8;  Length 447;
  Best Local Similarity   97.4%;  Pred. No. 3.1e-48;
  Matches  114;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117


RESULT 13
ADS87937
ID   ADS87937 standard; protein; 117 AA.
XX
AC   ADS87937;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:30.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
DR   N-PSDB; ADS87963.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 6; SEQ ID NO 30; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 117 AA;

  Query Match             95.2%;  Score 593;  DB 8;  Length 117;
  Best Local Similarity   96.6%;  Pred. No. 1.5e-47;
  Matches  113;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||||:|||| ||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSS 117


RESULT 14
ADS94934
ID   ADS94934 standard; protein; 117 AA.
XX
AC   ADS94934;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:30.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
```

```
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
DR   N-PSDB; ADS94960.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 8; SEQ ID NO 30; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 117 AA;

  Query Match           95.2%;  Score 593;  DB 8;  Length 117;
  Best Local Similarity   96.6%;  Pred. No. 1.5e-47;
  Matches  113;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSS 117


RESULT 15
ADS87939
ID   ADS87939 standard; protein; 447 AA.
XX
AC   ADS87939;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118* heavy chain SEQ ID NO:32.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 12; SEQ ID NO 32; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 447 AA;

  Query Match           95.2%;  Score 593;  DB 8;  Length 447;
  Best Local Similarity   96.6%;  Pred. No. 6.2e-47;
  Matches  113;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSS 117


Search completed: August 18, 2005, 06:09:10
Job time : 254.191 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 219.53 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-6
Perfect score: 623
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SGSYFYFDLWGRGTLVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	389.5	62.5	116	2	Q9UL89	Q9ul89 homo sapien
2	388.5	62.4	124	2	Q9UL92	Q9ul92 homo sapien
3	386	62.0	119	2	Q9UL94	Q9ul94 homo sapien
4	383	61.5	244	2	Q65ZC8	Q65zc8 homo sapien
5	380.5	61.1	498	2	Q6N041	Q6n041 homo sapien
6	379.5	60.9	118	2	Q9Z1C4	Q9z1c4 mus musculu
7	376	60.4	614	2	Q7TMT6	Q7tmt6 mus musculu
8	373	59.9	121	1	HV01_MOUSE	P01745 mus musculu
9	371	59.6	168	2	Q8VDC9	Q8vdc9 mus musculu
10	371	59.6	481	2	Q91WT1	Q91wt1 mus musculu
11	370.5	59.5	143	2	Q924Q0	Q924q0 mus musculu
12	369	59.2	144	2	Q924P5	Q924p5 mus musculu
13	369	59.2	470	2	Q7TMK1	Q7tmk1 mus musculu
14	365.5	58.7	159	2	Q96QS0	Q96qs0 homo sapien
15	365	58.6	125	2	Q9UL95	Q9ul95 homo sapien
16	363.5	58.3	145	2	Q924R3	Q924r3 mus musculu
17	363	58.3	147	2	Q925S3	Q925s3 mus musculu
18	362.5	58.2	143	2	Q91V67	Q91v67 mus musculu
19	362	58.1	473	2	Q9D8L4	Q9d8l4 mus musculu
20	361.5	58.0	613	2	Q8VCX7	Q8vcx7 mus musculu
21	359.5	57.7	469	2	Q7Z7P5	Q7z7p5 homo sapien
22	359	57.6	480	2	Q6P089	Q6p089 homo sapien
23	357.5	57.4	463	2	Q99LC4	Q99lc4 mus musculu
24	356	57.1	146	2	Q924R8	Q924r8 mus musculu
25	355.5	57.1	139	1	HV07_MOUSE	P01751 mus musculu
26	355.5	57.1	145	2	Q924Q7	Q924q7 mus musculu
27	354.5	56.9	518	2	Q6N030	Q6n030 homo sapien
28	354	56.8	474	2	Q8R3H6	Q8r3h6 mus musculu
29	353.5	56.7	143	2	Q924Q5	Q924q5 mus musculu
30	353	56.7	117	1	HV13_MOUSE	P01757 mus musculu
31	351.5	56.4	465	2	Q6PJB2	Q6pjb2 mus musculu
32	350.5	56.3	143	2	Q924R7	Q924r7 mus musculu
33	349.5	56.1	145	2	Q924R1	Q924r1 mus musculu
34	349	56.0	120	1	HV03_MOUSE	P01747 mus musculu
35	348.5	55.9	143	2	Q924P9	Q924p9 mus musculu
36	348.5	55.9	145	2	Q924R4	Q924r4 mus musculu
37	347.5	55.8	145	2	Q924P7	Q924p7 mus musculu
38	346.5	55.6	145	2	Q924Q6	Q924q6 mus musculu
39	346.5	55.6	145	2	Q924Q9	Q924q9 mus musculu
40	346	55.5	146	2	Q924Q3	Q924q3 mus musculu
41	345.5	55.5	143	2	Q91VA2	Q91va2 mus musculu
42	345.5	55.5	482	2	Q8K172	Q8k172 mus musculu
43	344	55.2	142	2	Q924Q1	Q924q1 mus musculu
44	344	55.2	464	2	Q6PF95	Q6pf95 mus musculu
45	343.5	55.1	500	2	Q9BRV0	Q9brv0 homo sapien

ALIGNMENTS

RESULT 1
Q9UL89
ID Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR PIR; PH0870; PH0870.
DR PIR; PH1671; PH1671.
DR HSSP; P01751; 1NQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 62.5%; Score 389.5; DB 2; Length 116;
Best Local Similarity 66.4%; Pred. No. 1.7e-31;
Matches 77; Conservative 13; Mismatches 23; Indels 3; Gaps 1;

```
Qy          5 VQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRYSPSF 64
              |||||||||| |:|:||| ||  |:|| | |||| ||:||| || | |      |: |
Db          1 VQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF 60

Qy         65 QGQVTISADKSISTAYLQWSSLKASDTAMYYCGS---GSYFYFDLWGRGTLVTVSS 117
              ||:|||:|||| ||||:: |||:: |||:||| |   | |:|||||||||||||
Db         61 QGRVTITADKSTSTAYMELSSLRSEDTAVYYCASSNWGPYWYFDLWGRGTLVTVSS 116
```

RESULT 2
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region

```
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;

  Query Match             62.4%;  Score 388.5;  DB 2;  Length 124;
  Best Local Similarity   59.7%;  Pred. No. 2.3e-31;
  Matches   74;  Conservative   17;  Mismatches   26;  Indels    7;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:|||||||||| |:|:||| ||| |:||:: |||| ||:||| |||| |     | |
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFY-------FDLWGRGTLV 113
              :  |||:||:: | | || |:: |||:: |||:|||  | |          || ||:||||
Db         61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGLYVVVPAAFSRFDYWGQGTLV 120

Qy        114 TVSS 117
              ||||
Db        121 TVSS 124


RESULT 3
Q9UL94
ID   Q9UL94      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL94;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035020; AAD56256.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13205 MW;  13E64F5345F4A16E CRC64;

  Query Match             62.0%;  Score 386;  DB 2;  Length 119;
  Best Local Similarity   62.2%;  Pred. No. 3.9e-31;
  Matches   74;  Conservative   17;  Mismatches   26;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||:|||||||||| |:|:||| ||| || |:: |||| ||:||| || | |     | |
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC--GSGSYFYFDLWGRGTLVTVSS 117
              :  |||:||:: | ||||||:: | |:: |||:|||  | |   :|| ||:||||||||
Db         61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLWFDPWGQGTLVTVSS 119


RESULT 4
Q65ZC8
ID   Q65ZC8      PRELIMINARY;      PRT;   244 AA.
AC   Q65ZC8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97362799; PubMed=9219263;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13057; CAA73500.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     244    244
SQ   SEQUENCE   244 AA;  26127 MW;  4B1F17868338F2BF CRC64;

  Query Match             61.5%;  Score 383;  DB 2;  Length 244;
  Best Local Similarity   60.3%;  Pred. No. 1.7e-30;
  Matches   73;  Conservative   23;  Mismatches   21;  Indels    4;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||||:|:|:||| ||| |: ::: |||| ||:||| || | | : |||:
Db          1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWVRQAPGQGLEWMGWIDPNNGDTRF 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFY-FDLWGRGTLVTVS 116
              :  |||:||:: | ||| ||:: | |:: |||:|||   |:||  |  |:||:|||||||
Db         61 AQRFQGRVTMTRDTSISAAYMEVSRLRSDDTAVYYCAREGTGSAIYGMDVWGQGTLVTVS 120

Qy        117 S 117
              |
Db        121 S 121


RESULT 5
Q6N041
ID   Q6N041      PRELIMINARY;      PRT;   498 AA.
AC   Q6N041;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686O16217 (Fragment).
GN   Name=DKFZp686O16217;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640710; CAE45829.1; -.
DR   HSSP; P01751; 1A6W.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   498 AA;  54125 MW;  40B3208A84E03B46 CRC64;

  Query Match             61.1%;  Score 380.5;  DB 2;  Length 498;
  Best Local Similarity   56.5%;  Pred. No. 6.2e-30;
  Matches   70;  Conservative   24;  Mismatches   23;  Indels    7;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||:||||| |:|:||| ||| ||:|:  |||| ||:| | ||:| | |  |:|
Db         35 QVQLVQSGADVKKPGASVKVSCKASGYTFTNYFFHWVRQAPGQGPEWMGMINPRDGSTKY 94

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC-------GSGSYFYFDLWGRGTLV 113
              :  |||:|::: | | || |:: |||:: ||||::|       |: : :||| ||:||||
Db         95 AQRFQGRVSMTRDTSTSTIYMELSSLRSEDTAMFFCARAGPGYGTSASYYFDYWGQGTLV 154

Qy        114 TVSS 117
              ||||
Db        155 TVSS 158


RESULT 6
Q9Z1C4
ID   Q9Z1C4      PRELIMINARY;      PRT;   118 AA.
AC   Q9Z1C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/c;
RX   MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.A., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Mol. Immunol. 34:441-452(1997).
DR   EMBL; U78801; AAD00293.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;

  Query Match             60.9%;  Score 379.5;  DB 2;  Length 118;
  Best Local Similarity   58.5%;  Pred. No. 1.7e-30;
  Matches   69;  Conservative   22;  Mismatches   26;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||: |||||: :|  |:|:||| ||||| |||: ||:| ||:||| :| ||||| || |
Db          1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY-FYFDLWGRGTLVTVSS 117
              :  |:|: |::|||| ||||:| ||| : |:|:|||   :   ||| ||:|| :||||
Db         61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYFDYWGQGTTLTVSS 118


RESULT 7
Q7TMT6
ID   Q7TMT6      PRELIMINARY;      PRT;   614 AA.
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MGC60843 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053409; AAH53409.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   614 AA;  67746 MW;  839BAF3B8D124F89 CRC64;

  Query Match             60.4%;  Score 376;  DB 2;  Length 614;
  Best Local Similarity   58.8%;  Pred. No. 2.2e-29;
  Matches   70;  Conservative   21;  Mismatches   26;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||| ||| |: ||| |:||||| ||| |:| |: ||:| |||||| :| :|||| || |
Db         20 QVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRVYPGDGDTNY 79
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Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS--GSYFYFDLWGRGTLVTVSS 117
               :  |:|: |::|||| ||||:| ||| : |:|:|:|    || : |  ||:|||||||:
Db          80 NGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDYGSSYRFAYWGQGTLVTVSA 138


RESULT 8
HV01_MOUSE
ID   HV01_MOUSE     STANDARD;      PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable region
RT   of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: This sequence was translated from an mRNA isolated
CC       from a myeloma that secretes IgG2b.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A93708; GVMS11.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;

  Query Match             59.9%;  Score 373;  DB 1;  Length 121;
  Best Local Similarity   56.2%;  Pred. No. 8.1e-30;
  Matches   68;  Conservative   22;  Mismatches   27;  Indels    4;  Gaps    1;

Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
               | || |||||: :|| |:||||| :|| ||:||||||:: || ||| :| ||||   | |
Db           1 EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60

Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYF----YFDLWGRGTLVTVS 116
               : : :|: |::|| | ||||:| ||| : |:|:|:|  | |:    ||| ||:|| :|||
Db          61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS 120

Qy         117 S 117
               |
Db         121 S 121


RESULT 9
Q8VDC9
ID   Q8VDC9       PRELIMINARY;      PRT;   168 AA.
AC   Q8VDC9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-MOG Z12 variable gamma 2a (Fragment).
GN   Name=IgG2a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Sembi P.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Chernajovsky Y.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416332; CAC94867.1; -.
DR   HSSP; P01863; 1E4W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     168    168
SQ   SEQUENCE   168 AA;  18293 MW;  1E3719FCC0E72723 CRC64;

  Query Match             59.6%;  Score 371;  DB 2;  Length 168;
  Best Local Similarity   58.0%;  Pred. No. 1.8e-29;
  Matches   69;  Conservative   20;  Mismatches   28;  Indels    2;  Gaps    1;

Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
               :||| |||||: ||| |:||||| :|| |:|||| ||:| || ||| :| | ||   | |
Db          20 QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIDWVKQRPGHGLEWIGEILPGSGRTNY 79

Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS--GSYFYFDLWGRGTLVTVSS 117
               :  |:|: | :|| | :|||:|:||| : |:|:||| :   | :|||:|| || |||||
Db          80 NEKFKGKTTFTADTSSNTAYIQFSSLTSEDSAVYYCANYGSSRWYFDVWGAGTTVTVSS 138


RESULT 10
Q91WT1
ID   Q91WT1       PRELIMINARY;      PRT;   481 AA.
AC   Q91WT1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013490; AAH13490.1; -.
DR   HSSP; P01751; 1A6W.
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DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   481 AA;  52105 MW;  97DF68D159463F65 CRC64;

  Query Match             59.6%;  Score 371;  DB 2;  Length 481;
  Best Local Similarity   58.1%;  Pred. No. 5.5e-29;
  Matches   68;  Conservative   23;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||:||| |: ||| |:||||| ||| ||||:| ||:| ||:||  :| ||||| :|:|
Db         20 QVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRPGQGLVWIGWIYPGDGNTKY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              :  |:|: |::|||| ||||:  ||| : |:|:|:|  |  : || ||:|| :||||
Db         80 NEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFCTRGGGWAFDYWGQGTTLTVSS 136


RESULT 11
Q924Q0
ID   Q924Q0      PRELIMINARY;      PRT;   143 AA.
AC   Q924Q0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   V165-D-J-C mu protein (Fragment).
GN   Name=V165-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069915; BAB63931.1; -.
DR   PIR; PH1159; PH1159.
DR   HSSP; P01751; 1A6W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     143    143
SQ   SEQUENCE   143 AA;  15704 MW;  C99D2433F2BAD8A0 CRC64;

  Query Match             59.5%;  Score 370.5;  DB 2;  Length 143;
  Best Local Similarity   57.6%;  Pred. No. 1.7e-29;
  Matches   68;  Conservative   19;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||| | |||: ||| |:|:||| ||| |||||| ||:| ||:||| :| ||||   | |
Db          1 QVQLQQPGAELVKPGASVKMSCKASGYTFTSYWITWVKQRPGQGLEWIGDIYPGSGSTNY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGS-YFYFDLWGRGTLVTVSS 117
              :  |: : |:: ||  ||||:| ||| : |:|:|||   | : ||| ||:|| :||||
Db         61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAPDSNHLYFDYWGQGTTLTVSS 118


RESULT 12
Q924P5
ID   Q924P5      PRELIMINARY;      PRT;   144 AA.
AC   Q924P5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069920; BAB63936.1; -.
DR   PIR; PH1137; PH1137.
DR   PIR; S26744; S26744.
DR   HSSP; P01751; 1A6W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  15865 MW;  CD07BE97E95C1B27 CRC64;

  Query Match             59.2%;  Score 369;  DB 2;  Length 144;
  Best Local Similarity   57.1%;  Pred. No. 2.5e-29;
  Matches   68;  Conservative   20;  Mismatches   29;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :||| | |||: ||| |:|:||| ||| |||||: ||:| ||:||| :| | |    |:|
Db          1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS--GSYFYFDLWGRGTLVTVSS 117
              :  |: : |:: ||  ||||:| ||| : |:|:||| |    ||:|||:|| || |||||
Db         61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCASYGSSYWYFDVWGTGTTVTVSS 119


RESULT 13
Q7TMK1
ID   Q7TMK1      PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
DR   HSSP; P01865; 1KB5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
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DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match            59.2%;  Score 369;  DB 2;  Length 470;
  Best Local Similarity  56.2%;  Pred. No. 8.5e-29;
  Matches   68;  Conservative   22;  Mismatches   27;  Indels    4;  Gaps    1;

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Db         80 NQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139

Qy        117 S 117
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Db        140 S 140


RESULT 14
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AC   Q96QS0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative matrix cell adhesion molecule-3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tilson M.D.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY039025; AAK82649.1; -.
DR   HSSP; P01869; 1AE6.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   159 AA;  17497 MW;  5D29537E881FAF02 CRC64;

  Query Match            58.7%;  Score 365.5;  DB 2;  Length 159;
  Best Local Similarity  53.1%;  Pred. No. 6.2e-29;
  Matches   69;  Conservative   21;  Mismatches   27;  Indels   13;  Gaps    2;

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              :|||||||||||||| |:|:||| ||| |::|:: |||| ||:| | ||:| |     ||
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC------------GSGSYFY-FDLW 107
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Db         80 SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFYYYGMDVW 139

Qy        108 GRGTLVTVSS 117
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RESULT 15
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AC   Q9UL95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035019; AAD56255.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  13516 MW;  0D3CD5C232488EAC CRC64;

  Query Match            58.6%;  Score 365;  DB 2;  Length 125;
  Best Local Similarity  56.8%;  Pred. No. 5.4e-29;
  Matches   71;  Conservative   19;  Mismatches   27;  Indels    8;  Gaps    2;

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Qy        113 VTVSS 117
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Db        121 VTVSS 125


Search completed: August 18, 2005, 06:18:08
Job time : 221.53 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 221.597 Seconds
(without alignments)
206.752 Million cell updates/sec

Title: US-10-684-957-6
Perfect score: 623
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SGSYFYFDLWGRGTLVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	623	100.0	117	17	US-10-684-957-6	Sequence 6, Appli
2	623	100.0	447	17	US-10-684-957-17	Sequence 17, Appl
3	618	99.2	117	17	US-10-684-957-14	Sequence 14, Appl
4	612	98.2	447	17	US-10-684-957-21	Sequence 21, Appl
5	607	97.4	117	17	US-10-684-957-10	Sequence 10, Appl
6	607	97.4	447	17	US-10-684-957-19	Sequence 19, Appl
7	593	95.2	117	17	US-10-684-957-30	Sequence 30, Appl
8	593	95.2	447	17	US-10-684-957-32	Sequence 32, Appl
9	566	90.9	118	17	US-10-726-332-145	Sequence 145, App
10	565	90.7	118	17	US-10-726-332-134	Sequence 134, App
11	565	90.7	225	16	US-10-128-520-162	Sequence 162, App
12	564.5	90.6	126	14	US-10-041-860-313	Sequence 313, App
13	563.5	90.4	126	14	US-10-041-860-27	Sequence 27, Appl
14	563.5	90.4	126	14	US-10-041-860-214	Sequence 214, App
15	563.5	90.4	126	14	US-10-041-860-249	Sequence 249, App
16	563.5	90.4	126	16	US-10-665-383-34	Sequence 34, Appl
17	562	90.2	118	17	US-10-726-332-135	Sequence 135, App
18	561	90.0	125	17	US-10-891-658-79	Sequence 79, Appl
19	560.5	90.0	226	16	US-10-128-520-179	Sequence 179, App
20	559.5	89.8	126	14	US-10-041-860-35	Sequence 35, Appl
21	559.5	89.8	126	14	US-10-041-860-216	Sequence 216, App
22	559.5	89.8	126	14	US-10-041-860-251	Sequence 251, App
23	559.5	89.8	126	14	US-10-041-860-337	Sequence 337, App
24	559.5	89.8	126	16	US-10-665-383-50	Sequence 50, Appl
25	559	89.7	118	17	US-10-726-332-143	Sequence 143, App
26	558.5	89.6	224	16	US-10-128-520-170	Sequence 170, App
27	557.5	89.5	126	14	US-10-041-860-23	Sequence 23, Appl
28	557.5	89.5	126	14	US-10-041-860-248	Sequence 248, App
29	557.5	89.5	126	14	US-10-041-860-300	Sequence 300, App
30	557.5	89.5	126	16	US-10-665-383-26	Sequence 26, Appl
31	557.5	89.5	224	16	US-10-128-520-181	Sequence 181, App
32	557	89.4	225	16	US-10-128-520-166	Sequence 166, App
33	556	89.2	118	17	US-10-726-332-30	Sequence 30, Appl
34	556	89.2	118	17	US-10-726-332-141	Sequence 141, App
35	555.5	89.2	224	16	US-10-128-520-180	Sequence 180, App
36	554.5	89.0	120	14	US-10-125-687-6	Sequence 6, Appli
37	554.5	89.0	120	18	US-10-996-191-6	Sequence 6, Appli
38	554	88.9	225	16	US-10-128-520-178	Sequence 178, App
39	553.5	88.8	224	16	US-10-128-520-167	Sequence 167, App
40	553	88.8	123	15	US-10-173-551-4	Sequence 4, Appli
41	553	88.8	225	16	US-10-128-520-158	Sequence 158, App
42	552.5	88.7	224	16	US-10-128-520-164	Sequence 164, App
43	552.5	88.7	224	16	US-10-128-520-182	Sequence 182, App
44	551.5	88.5	224	16	US-10-128-520-176	Sequence 176, App
45	551	88.4	118	17	US-10-726-332-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-684-957-6
; Sequence 6, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-6

Query Match 100.0%; Score 623; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-684-957-17
; Sequence 17, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-684-957-17

  Query Match           100.0%;  Score 623;  DB 17;  Length 447;
  Best Local Similarity  100.0%;  Pred. No. 5.9e-51;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-10-684-957-14
; Sequence 14, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-14

  Query Match           99.2%;  Score 618;  DB 17;  Length 117;
  Best Local Similarity  99.1%;  Pred. No. 4.4e-51;
  Matches  116;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
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Db          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117


RESULT 4
US-10-684-957-21
; Sequence 21, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-21

  Query Match           98.2%;  Score 612;  DB 17;  Length 447;
  Best Local Similarity  98.3%;  Pred. No. 6.6e-50;
  Matches  115;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db           1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

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RESULT 5
US-10-684-957-10
; Sequence 10, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-10

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  Best Local Similarity   97.4%;  Pred. No. 4.9e-50;
  Matches  114;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117


RESULT 6
US-10-684-957-19
; Sequence 19, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-19

  Query Match             97.4%;  Score 607;  DB 17;  Length 447;
  Best Local Similarity   97.4%;  Pred. No. 2e-49;
  Matches  114;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLWGRGTLVTVSS 117


RESULT 7
US-10-684-957-30
; Sequence 30, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-684-957-30

  Query Match             95.2%;  Score 593;  DB 17;  Length 117;
  Best Local Similarity   96.6%;  Pred. No. 1.1e-48;
  Matches  113;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSS 117


RESULT 8
US-10-684-957-32
; Sequence 32, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-32

  Query Match             95.2%;  Score 593;  DB 17;  Length 447;
  Best Local Similarity   96.6%;  Pred. No. 4.2e-48;
  Matches  113;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYWYFDLRGRGTLVTVSS 117


RESULT 9
US-10-726-332-145
; Sequence 145, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
```

```
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-145

  Query Match             90.9%;  Score 566;  DB 17;  Length 118;
  Best Local Similarity   92.3%;  Pred. No. 3.9e-46;
  Matches  108;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||    |  ||| ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHSGSYFDYWGQGTLVTVSS 117


RESULT 10
US-10-726-332-134
; Sequence 134, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 134
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 101, 102
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-10-726-332-134

  Query Match             90.7%;  Score 565;  DB 17;  Length 118;
  Best Local Similarity   90.6%;  Pred. No. 4.9e-46;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||    |  ||| ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGGXXAFDIWGQGTMVTVSS 117


RESULT 11
US-10-128-520-162
; Sequence 162, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
;  APPLICANT: PAN et al.
;  TITLE OF INVENTION: Human TIMP-1 Antibodies
;  FILE REFERENCE: 02973.00073
;  CURRENT APPLICATION NUMBER: US/10/128,520
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: US 60/285,683
;  PRIOR FILING DATE: 2001-04-24
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 162
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-520-162

  Query Match             90.7%;  Score 565;  DB 16;  Length 225;
  Best Local Similarity   89.3%;  Pred. No. 9.6e-46;
  Matches  108;  Conservative    4;  Mismatches    5;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS----GSYFYFDLWGRGTLVTVS 116
              ||||||||||||||||||||||||||||||||||||||      |  ||||:||:|||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARFRAYGDDFYFDVWGQGTLVTVS 120

Qy        117 S 117
              |
Db        121 S 121


RESULT 12
US-10-041-860-313
; Sequence 313, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 313
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-313

  Query Match             90.6%;  Score 564.5;  DB 14;  Length 126;
  Best Local Similarity   87.3%;  Pred. No. 5.9e-46;
  Matches  110;  Conservative    3;  Mismatches    4;  Indels    9;  Gaps    2;
```

```
Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFY--------FDLWGRGT 111
              |||||||||||||||||||||||||||||||||||||   |||:|         || ||:||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSETYYNVFDYWGQGT 120

Qy        112 LVTVSS 117
              ||||||
Db        121 LVTVSS 126


RESULT 13
US-10-041-860-27
; Sequence 27, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-27

  Query Match             90.4%;  Score 563.5;  DB 14;  Length 126;
  Best Local Similarity   87.3%;  Pred. No. 7.3e-46;
  Matches  110;  Conservative    2;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFY--------FDLWGRGT 111
              |||||||||||||||||||||||||||||||||||||   |||:|         || ||:||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSETYYNVFDYWGQGT 120

Qy        112 LVTVSS 117
              ||||||
Db        121 LVTVSS 126


RESULT 14
US-10-041-860-214
; Sequence 214, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 214
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-214

  Query Match             90.4%;  Score 563.5;  DB 14;  Length 126;
  Best Local Similarity   87.3%;  Pred. No. 7.3e-46;
  Matches  110;  Conservative    2;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFY--------FDLWGRGT 111
              |||||||||||||||||||||||||||||||||||||   |||:|         || ||:||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSETYYNVFDYWGQGT 120

Qy        112 LVTVSS 117
              ||||||
Db        121 LVTVSS 126


RESULT 15
US-10-041-860-249
; Sequence 249, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 249
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-249

  Query Match             90.4%;  Score 563.5;  DB 14;  Length 126;
  Best Local Similarity   87.3%;  Pred. No. 7.3e-46;
  Matches  110;  Conservative    2;  Mismatches    5;  Indels    9;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG-SGSYFY--------FDLWGRGT 111
              |||||||||||||||||||||||||||||||||||||   |||:|         || ||:||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSETYYNVFDYWGQGT 120

Qy        112 LVTVSS 117
              ||||||
Db        121 LVTVSS 126


Search completed: August 18, 2005, 07:08:02
Job time : 221.722 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 202.643 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-8
Perfect score: 556
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQRSGGSSFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	516	92.8	109	2	Q9UL86	Q9ul86 homo sapien
2	512	92.1	129	1	KV3L_HUMAN	P18135 homo sapien
3	512	92.1	129	1	KV3M_HUMAN	P18136 homo sapien
4	508	91.4	109	2	Q9UL78	Q9ul78 homo sapien
5	504	90.6	109	1	KV3B_HUMAN	P01620 homo sapien
6	502	90.3	235	2	Q6PJF2	Q6pjf2 homo sapien
7	501	90.1	109	1	KV3E_HUMAN	P01623 homo sapien
8	497	89.4	109	1	KV3D_HUMAN	P01622 homo sapien
9	488.5	87.9	236	2	Q6PIL8	Q6pil8 homo sapien
10	484	87.1	108	1	KV3A_HUMAN	P01619 homo sapien
11	477.5	85.9	236	2	Q6P5S8	Q6p5s8 homo sapien
12	476	85.6	109	1	KV3G_HUMAN	P04206 homo sapien
13	472	84.9	235	2	Q6GMV9	Q6gmv9 homo sapien
14	462	83.1	100	1	KV3C_HUMAN	P01621 homo sapien
15	445.5	80.1	108	2	Q9UL83	Q9ul83 homo sapien
16	443.5	79.8	128	1	KV3K_HUMAN	P06311 homo sapien
17	431	77.5	109	1	KV3F_HUMAN	P01624 homo sapien
18	429	77.2	129	1	KV3H_HUMAN	P04207 homo sapien
19	419	75.4	116	1	KV3J_HUMAN	P04434 homo sapien
20	418.5	75.3	115	1	KV3I_HUMAN	P04433 homo sapien
21	417	75.0	109	2	Q9UL85	Q9ul85 homo sapien
22	415	74.6	235	2	Q6GMW0	Q6gmw0 homo sapien
23	400.5	72.0	236	2	Q6GMX8	Q6gmx8 homo sapien
24	397.5	71.5	108	2	Q9UL77	Q9ul77 homo sapien
25	387	69.6	107	2	Q96SA9	Q96sa9 homo sapien
26	385.5	69.3	114	1	KV4A_HUMAN	P01625 homo sapien
27	383.5	69.0	134	1	KV4C_HUMAN	P06314 homo sapien
28	383	68.9	107	2	Q9UL81	Q9ul81 homo sapien
29	382	68.7	107	1	KV1D_HUMAN	P01596 homo sapien
30	380.5	68.4	236	2	Q6PIH7	Q6pih7 homo sapien
31	376.5	67.7	108	1	KV1H_HUMAN	P01600 homo sapien
32	376.5	67.7	255	2	Q6KB05	Q6kb05 mus musculu
33	372.5	67.0	108	2	Q9UL70	Q9ul70 homo sapien
34	372	66.9	133	1	KV4B_HUMAN	P06313 homo sapien
35	370.5	66.6	108	1	KV1E_HUMAN	P01597 homo sapien
36	370.5	66.6	108	2	Q9UL79	Q9ul79 homo sapien
37	368.5	66.3	111	1	KV3M_MOUSE	P01665 mus musculu
38	367.5	66.1	108	1	KV1M_HUMAN	P01605 homo sapien
39	367.5	66.1	129	1	KV1W_HUMAN	P04431 homo sapien
40	366.5	65.9	236	2	Q6GMW1	Q6gmw1 homo sapien
41	365.5	65.7	108	1	KV1F_HUMAN	P01598 homo sapien
42	363.5	65.4	108	1	KV1K_HUMAN	P01603 homo sapien
43	362.5	65.2	108	1	KV1Y_HUMAN	P80362 homo sapien
44	361.5	65.0	111	1	KV3L_MOUSE	P01664 mus musculu
45	361.5	65.0	111	1	KV3O_MOUSE	P01667 mus musculu

ALIGNMENTS

RESULT 1
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSSP; P01625; 1EK3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 92.8%; Score 516; DB 2; Length 109;
Best Local Similarity 93.5%; Pred. No. 2.2e-44;
Matches 101; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||| |||||||||||||||||||||||||||||||||||| ||||||||
Db          1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||| ||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108
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RESULT 2
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       Ig kappa chain V-III region HAH.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     55       Complementarity-determining-1.
FT   DOMAIN      56     70       Framework-2.
FT   DOMAIN      71     77       Complementarity-determining-2.
FT   DOMAIN      78    109       Framework-3.
FT   DOMAIN     110    118       Complementarity-determining-3.
FT   DOMAIN     119    129       JK1 segment.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             92.1%;  Score 512;  DB 1;  Length 129;
  Best Local Similarity   93.5%;  Pred. No. 6.8e-44;
  Matches  101;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | |  ||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPRTFGQGTKVEIK 128


RESULT 3
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0021; K3HUHI.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       Ig kappa chain V-III region HIC.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     55       Complementarity-determining-1.
FT   DOMAIN      56     70       Framework-2.
FT   DOMAIN      71     77       Complementarity-determining-2.
FT   DOMAIN      78    109       Framework-3.
FT   DOMAIN     110    118       Complementarity-determining-3.
FT   DOMAIN     119    129       JK1 segment.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14070 MW;  7395528EA2BB74D6 CRC64;

  Query Match             92.1%;  Score 512;  DB 1;  Length 129;
  Best Local Similarity   92.6%;  Pred. No. 6.8e-44;
  Matches  100;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||| |||||||: | | :||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLEPXDFAVYYCQQYGSSPWTFGQGTKVEIK 128


RESULT 4
Q9UL78
ID   Q9UL78      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
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DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; H44151; H44151.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0964; PH0964.
DR   PIR; PH0965; PH0965.
DR   PIR; S33988; S33988.
DR   PIR; S34096; S34096.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             91.4%;  Score 508;  DB 2;  Length 109;
  Best Local Similarity   92.6%;  Pred. No. 1.4e-43;
  Matches  100;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||| |||||: | |  ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108


RESULT 5
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01892; K3HUSI.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match             90.6%;  Score 504;  DB 1;  Length 109;
  Best Local Similarity   90.7%;  Pred. No. 3.6e-43;
  Matches   98;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||:|||||||: | |  ||| |:||:||
Db         61 DRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPQTFGQGSKVEIK 108


RESULT 6
Q6PJF2
ID   Q6PJF2      PRELIMINARY;      PRT;   235 AA.
AC   Q6PJF2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016380; AAH16380.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match             90.3%;  Score 502;  DB 2;  Length 235;
  Best Local Similarity   89.8%;  Pred. No. 1.4e-42;
  Matches   97;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||| |||||||||||||||| |||:|||||||||||||||::|:||||||||
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Db         21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||: | |  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDIK 128


RESULT 7
KV3E_HUMAN
ID   KV3E_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01623;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region WOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11746 MW;  566C115E6B9CBEEE CRC64;

  Query Match             90.1%;  Score 501;  DB 1;  Length 109;
  Best Local Similarity   90.7%;  Pred. No. 7.3e-43;
  Matches   98;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSGYLGWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||: |    ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108


RESULT 8
KV3D_HUMAN
ID   KV3D_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01622;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region Ti.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   Ti). IV. The complete amino acid sequence and its significance for the
RT   mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01895; K3HUTI.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11788 MW;  8C35058CDC7749BC CRC64;

  Query Match             89.4%;  Score 497;  DB 1;  Length 109;
  Best Local Similarity   89.8%;  Pred. No. 1.9e-42;
  Matches   97;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||:|:|||||||||||||||| |||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||: | |  ||| ||||::|
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPSTFGQGTKVELK 108


RESULT 9
Q6PIL8
ID   Q6PIL8      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
```

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032451; AAH32451.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match             87.9%;  Score 488.5;  DB 2;  Length 236;
  Best Local Similarity   89.0%;  Pred. No. 3.2e-41;
  Matches   97;  Conservative    4;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              | |||||||||||||||||||||||||:||||||||||||||||||| ||||||||
Db         21 ENVLTQSPGTLSLSPGERATLSCRASQSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | |   ||| ||::|||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDIK 129


RESULT 10
KV3A_HUMAN
ID   KV3A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01619;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-III region B6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   PubMed=11946339;
RA   Milstein C.;
RT   "The basic sequences of immunoglobulin kappa chains: sequence studies
RT   of Bence Jones proteins Rad, Fr4 and B6.";
RL   FEBS Lett. 2:301-304(1969).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01891; K3HUB6.
DR   HSSP; P01625; 1EEQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11635 MW;  8BC14FF07A419E3D CRC64;

  Query Match             87.1%;  Score 484;  DB 1;  Length 108;
  Best Local Similarity   82.4%;  Pred. No. 3.8e-41;
  Matches   89;  Conservative   11;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :||||:||||||||||:|| ||||||||:| :||||||||||||||||:|| |||||||||
Db          1 ZIVLTZSPGTLSLSPGZRAALSCRASQSLSGNYLAWYQQKPGQAPRLLMYGVSSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||| |||||||||:|||||||||: | | |||| |:|::||
Db         61 DRFSGSGSGADFTLTISRLZPEDFAVYYCQQYGSSPFTFGQGSKLEIK 108


RESULT 11
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match             85.9%;  Score 477.5;  DB 2;  Length 236;
  Best Local Similarity   86.2%;  Pred. No. 4.1e-40;
  Matches   94;  Conservative    8;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||| ||||||||||||||:| ||:||||||:||||||||||||||||||||
Db         21 EIVLTQSPGTLSFSPGERATLSCRASQTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIK 108
              ||||||||||||||||:||||||||||:||: | | | ||| ||:|:||
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Db         81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQQYGTSPSLTFGGGTRVEIK 129


RESULT 12
KV3G_HUMAN
ID   KV3G_HUMAN     STANDARD;      PRT;   109 AA.
AC   P04206;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region GOL (Rheumatoid factor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA   Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT   "Amino acid sequence of a light chain variable region of a human
RT   rheumatoid factor of the Wa idiotypic group, in part predicted by its
RT   reactivity with antipeptide antibodies.";
RL   Mol. Immunol. 23:239-244(1986).
DR   PIR; A01893; K3HUGO.
DR   HSSP; P01625; 1EK3.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11830 MW;  9349A5B1D93588B6 CRC64;

  Query Match             85.6%;  Score 476;  DB 1;  Length 109;
  Best Local Similarity   86.1%;  Pred. No. 2.5e-40;
  Matches   93;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||:   |  ||||||||||||||||:||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRAALLSSRGYLAWYQQKPGQAPRLLMYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | |  :|| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRSFGQGTKVEIK 108


RESULT 13
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             84.9%;  Score 472;  DB 2;  Length 235;
  Best Local Similarity   85.2%;  Pred. No. 1.5e-39;
  Matches   92;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||| |||||||||:| ||||||||||||||||:| || ||||||
Db         21 EIVLTQSPGTLSLSPGERAALSCRASQSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||| ||||:|:||: | |  ||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGTSPLTFGGGTKVEIK 128


RESULT 14
KV3C_HUMAN
ID   KV3C_HUMAN     STANDARD;      PRT;   100 AA.
AC   P01621;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region NG9 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093600; PubMed=6419127;
RA   Bentley D.L.;
RT   "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RT   a small family of germ-line V genes.";
RL   Nature 307:77-80(1984).
CC   -!- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.
DR   PIR; A01894; K3HUNG.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
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```
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1      4
FT   CHAIN         5    100       Ig kappa chain V-III region NG9.
FT   DISULFID     27     93       By similarity.
FT   NON_TER     100    100
SQ   SEQUENCE   100 AA;  10729 MW;  5D9AF363CC52632F CRC64;

  Query Match             83.1%;  Score 462;  DB 1;  Length 100;
  Best Local Similarity   94.7%;  Pred. No. 5.8e-39;
  Matches   90;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db          5 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGATSRATGIP 64

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS 95
              |||||| |||||||||||||||||||: | |
Db         65 DRFSGSASGTDFTLTISRLEPEDFAVYYCQQYGNS 99


RESULT 15
Q9UL83
ID   Q9UL83      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035031; AAD56267.1; -.
DR   PIR; B30609; B30609.
DR   PIR; C30609; C30609.
DR   PIR; D30609; D30609.
DR   PIR; S34098; S34098.
DR   PIR; S34099; S34099.
DR   HSSP; P01625; 1LVE.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

  Query Match             80.1%;  Score 445.5;  DB 2;  Length 108;
  Best Local Similarity   83.3%;  Pred. No. 2.9e-37;
  Matches   90;  Conservative    6;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:|||| |||:|||||||||||||||: ||||||||||||||| ||:||||||
Db          1 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQQKPGQAPRLLIYCASTRATGIP 59

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||:|||||| |: |||||||||      ||||||||||||
Db         60 ARFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107
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Search completed: August 18, 2005, 06:18:09
Job time : 203.643 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 232.792 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-8
Perfect score: 556
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQRSGGSSFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	556	100.0	108	8	ADS87923	Ads87923 Anti-IFN-
2	556	100.0	108	8	ADS87915	Ads87915 Anti-IFN-
3	556	100.0	108	8	ADS94920	Ads94920 Anti-IFN-
4	556	100.0	108	8	ADS94912	Ads94912 Anti-IFN-
5	556	100.0	215	8	ADS87929	Ads87929 Anti-IFN-
6	556	100.0	215	8	ADS87925	Ads87925 Anti-IFN-
7	556	100.0	215	8	ADS94926	Ads94926 Anti-IFN-
8	556	100.0	215	8	ADS94922	Ads94922 Anti-IFN-
9	547	98.4	108	8	ADS87919	Ads87919 Anti-IFN-
10	547	98.4	108	8	ADS94916	Ads94916 Anti-IFN-
11	547	98.4	215	8	ADS87927	Ads87927 Anti-IFN-
12	547	98.4	215	8	ADS94924	Ads94924 Anti-IFN-
13	531	95.5	108	7	ADK18802	Adk18802 Anti-huma
14	531	95.5	108	7	ADK18836	Adk18836 Anti-huma
15	531	95.5	108	7	ADK18623	Adk18623 Anti-huma
16	531	95.5	108	7	ADK18945	Adk18945 Anti-huma
17	531	95.5	108	8	ADL25462	Adl25462 Human mAb
18	524.5	94.3	110	8	ADP47298	Adp47298 Human pho
19	524.5	94.3	224	4	AAB99375	Aab99375 Human int
20	524.5	94.3	224	4	AAB75008	Aab75008 Anti-IL8
21	522.5	94.0	226	4	AAB99378	Aab99378 Human int
22	522.5	94.0	226	4	AAB75011	Aab75011 Anti-IL8
23	519	93.3	384	4	AAU14462	Aau14462 Human nov
24	519	93.3	384	4	AAU14463	Aau14463 Human nov
25	519	93.3	384	4	AAU14461	Aau14461 Human nov
26	519	93.3	384	4	AAU14464	Aau14464 Human nov
27	519	93.3	384	8	ADH80782	Adh80782 Human pol
28	518.5	93.3	224	4	AAB99392	Aab99392 Human int
29	518.5	93.3	224	4	AAB75025	Aab75025 Anti-IL8
30	518.5	93.3	226	4	AAB99390	Aab99390 Human int
31	518.5	93.3	226	4	AAB75023	Aab75023 Anti-IL8
32	518	93.2	108	8	ADQ16703	Adq16703 Modified
33	518	93.2	109	8	ADP46971	Adp46971 Murine li
34	518	93.2	120	7	ADD40551	Add40551 3E1/4G11
35	518	93.2	215	8	ADQ16702	Adq16702 Modified
36	517.5	93.1	224	4	AAB99377	Aab99377 Human int
37	517.5	93.1	224	4	AAB75010	Aab75010 Anti-IL8
38	517	93.0	129	2	AAR38672	Aar38672 vk325-Jk2
39	517	93.0	384	8	ADH80779	Adh80779 Human pol
40	517	93.0	384	8	ADH80781	Adh80781 Human pol
41	517	93.0	385	8	ADH80780	Adh80780 Human pol
42	516.5	92.9	226	4	AAB99376	Aab99376 Human int
43	516.5	92.9	226	4	AAB75009	Aab75009 Anti-IL8
44	516	92.8	109	8	ADP47295	Adp47295 Human pho
45	515.5	92.7	224	4	AAB99379	Aab99379 Human int

ALIGNMENTS

RESULT 1
ADS87923
ID ADS87923 standard; protein; 108 AA.
XX
AC ADS87923;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:16.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87922.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 9; SEQ ID NO 16; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising

```
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 108 AA;

  Query Match             100.0%;  Score 556;  DB 8;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-34;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 2
ADS87915
ID   ADS87915 standard; protein; 108 AA.
XX
AC   ADS87915;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody light chain variable region SEQ ID NO:8.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
DR   N-PSDB; ADS87914.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 9; SEQ ID NO 8; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 108 AA;

  Query Match             100.0%;  Score 556;  DB 8;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-34;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 3
ADS94920
ID   ADS94920 standard; protein; 108 AA.
XX
AC   ADS94920;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody light chain variable region SEQ ID NO:16.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
```

PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94919.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 11; SEQ ID NO 16; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 108 AA;

```
  Query Match             100.0%;  Score 556;  DB 8;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-34;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
```

RESULT 4
ADS94912
ID ADS94912 standard; protein; 108 AA.
XX
AC ADS94912;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:8.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94911.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 11; SEQ ID NO 8; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 108 AA;

```
  Query Match             100.0%;  Score 556;  DB 8;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-34;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
```

RESULT 5
ADS87929
ID ADS87929 standard; protein; 215 AA.
XX
AC ADS87929;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 light chain SEQ ID NO:22.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;

KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 22; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 556; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.5e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108

RESULT 6
ADS87925
ID ADS87925 standard; protein; 215 AA.
XX
AC ADS87925;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 light chain SEQ ID NO:18.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 18; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 556; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.5e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108

RESULT 7
ADS94926
ID ADS94926 standard; protein; 215 AA.
XX
AC ADS94926;
XX

DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 light chain SEQ ID NO:22.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 22; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

```
  Query Match             100.0%;  Score 556;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-34;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
```

RESULT 8
ADS94922
ID ADS94922 standard; protein; 215 AA.
XX
AC ADS94922;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 light chain SEQ ID NO:18.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 18; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

```
  Query Match             100.0%;  Score 556;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-34;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 9
ADS87919
ID   ADS87919 standard; protein; 108 AA.
XX
AC   ADS87919;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody light chain variable region SEQ ID NO:12.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
DR   N-PSDB; ADS87918.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 9; SEQ ID NO 12; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 108 AA;

  Query Match             98.4%;  Score 547;  DB 8;  Length 108;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-33;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 10
ADS94916
ID   ADS94916 standard; protein; 108 AA.
XX
AC   ADS94916;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody light chain variable region SEQ ID NO:12.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
DR   N-PSDB; ADS94915.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 11; SEQ ID NO 12; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
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CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 108 AA;

  Query Match             98.4%;  Score 547;  DB 8;  Length 108;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-33;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 11
ADS87927
ID   ADS87927 standard; protein; 215 AA.
XX
AC   ADS87927;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118 or 1118* light chain SEQ ID NO:20.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 15; SEQ ID NO 20; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 215 AA;

  Query Match             98.4%;  Score 547;  DB 8;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 4.4e-33;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 12
ADS94924
ID   ADS94924 standard; protein; 215 AA.
XX
AC   ADS94924;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody 1118 or 1118* light chain SEQ ID NO:20.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035747-A2.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-US032871.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
PA   (MEDA-) MEDAREX INC.
XX
PI   Welcher AA,  Chute HT,  Li Y,  Huang H;
XX
DR   WPI; 2004-348443/32.
XX
PT   New human anti-interferon-gamma neutralizing antibodies for treating
PT   interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT   diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT   rejection.
XX
PS   Claim 17; SEQ ID NO 20; 115pp; English.
```

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XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS94940) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 215 AA;

  Query Match             98.4%;  Score 547;  DB 8;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 4.4e-33;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 13
ADK18802
ID   ADK18802 standard; protein; 108 AA.
XX
AC   ADK18802;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #28.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF,  Jia X,  Feng X,  Yang X,  Chen F,  Gazit G,  Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 226; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 108 AA;

  Query Match             95.5%;  Score 531;  DB 7;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 3.7e-32;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

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RESULT 14
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ID   ADK18836 standard; protein; 108 AA.
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AC   ADK18836;
XX
DT   06-MAY-2004  (first entry)
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DE   Anti-human PDGF-D antibody protein related sequence #62.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
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PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF,  Jia X,  Feng X,  Yang X,  Chen F,  Gazit G,  Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 260; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
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ID   ADK18623 standard; protein; 108 AA.
XX
AC   ADK18623;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Anti-human PDGF-D antibody light chain protein sequence.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF,  Jia X,  Feng X,  Yang X,  Chen F,  Gazit G,  Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 47; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 108 AA;

  Query Match             95.5%;  Score 531;  DB 7;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 3.7e-32;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 204.551 Seconds
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206.752 Million cell updates/sec

Title: US-10-684-957-8
Perfect score: 556
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQRSGGSSFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	556	100.0	108	17	US-10-684-957-8	Sequence 8, Appli
2	556	100.0	108	17	US-10-684-957-16	Sequence 16, Appl
3	556	100.0	215	17	US-10-684-957-18	Sequence 18, Appl
4	556	100.0	215	17	US-10-684-957-22	Sequence 22, Appl
5	547	98.4	108	17	US-10-684-957-12	Sequence 12, Appl
6	547	98.4	215	17	US-10-684-957-20	Sequence 20, Appl
7	535	96.2	108	15	US-10-292-088-113	Sequence 113, App
8	531	95.5	108	14	US-10-041-860-47	Sequence 47, Appl
9	531	95.5	108	14	US-10-041-860-226	Sequence 226, App
10	531	95.5	108	14	US-10-041-860-260	Sequence 260, App
11	531	95.5	108	14	US-10-041-860-369	Sequence 369, App
12	531	95.5	108	16	US-10-665-383-72	Sequence 72, Appl
13	524.5	94.3	110	17	US-10-726-332-213	Sequence 213, App
14	524.5	94.3	224	10	US-09-453-234-52	Sequence 52, Appl
15	524	94.2	109	17	US-10-706-689-39	Sequence 39, Appl
16	524	94.2	109	18	US-10-988-360-39	Sequence 39, Appl
17	522.5	94.0	226	10	US-09-453-234-42	Sequence 42, Appl
18	519	93.3	384	15	US-10-291-265-804	Sequence 804, App
19	519	93.3	384	15	US-10-291-265-805	Sequence 805, App
20	519	93.3	384	15	US-10-291-265-806	Sequence 806, App
21	519	93.3	384	15	US-10-291-265-807	Sequence 807, App
22	518.5	93.3	224	10	US-09-453-234-76	Sequence 76, Appl
23	518.5	93.3	226	10	US-09-453-234-72	Sequence 72, Appl
24	518	93.2	108	15	US-10-307-724-123	Sequence 123, App
25	518	93.2	108	16	US-10-737-290-123	Sequence 123, App
26	518	93.2	109	17	US-10-725-962-27	Sequence 27, Appl
27	518	93.2	120	17	US-10-506-743-2	Sequence 2, Appli
28	518	93.2	130	16	US-10-737-290-161	Sequence 161, App
29	518	93.2	215	15	US-10-307-724-122	Sequence 122, App
30	518	93.2	215	16	US-10-737-290-122	Sequence 122, App
31	518	93.2	239	16	US-10-737-290-142	Sequence 142, App
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34	517	93.0	128	17	US-10-910-901-18	Sequence 18, Appl
35	516.5	92.9	226	10	US-09-453-234-38	Sequence 38, Appl
36	516	92.8	109	17	US-10-726-332-210	Sequence 210, App
37	516	92.8	109	17	US-10-938-353-114	Sequence 114, App
38	516	92.8	235	17	US-10-938-353-60	Sequence 60, Appl
39	515.5	92.7	224	10	US-09-453-234-44	Sequence 44, Appl
40	515.5	92.7	224	10	US-09-453-234-78	Sequence 78, Appl
41	515	92.6	108	15	US-10-269-711-21	Sequence 21, Appl
42	515	92.6	108	16	US-10-684-109-21	Sequence 21, Appl
43	514.5	92.5	107	15	US-10-292-088-84	Sequence 84, Appl
44	514.5	92.5	234	15	US-10-292-088-88	Sequence 88, Appl
45	514	92.4	108	9	US-09-948-939-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-684-957-8
; Sequence 8, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-8

Query Match 100.0%; Score 556; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 2e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-684-957-16
; Sequence 16, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-16

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  Best Local Similarity  100.0%;  Pred. No. 2e-39;
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RESULT 3
US-10-684-957-18
; Sequence 18, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-18

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US-10-684-957-22
; Sequence 22, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-22

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; Sequence 12, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
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;   ORGANISM: Homo sapiens
US-10-684-957-12

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; Sequence 20, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-20

  Query Match             98.4%;  Score 547;  DB 17;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-38;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108


RESULT 7
US-10-292-088-113
; Sequence 113, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-113

  Query Match             96.2%;  Score 535;  DB 15;  Length 108;
  Best Local Similarity   96.3%;  Pred. No. 1.2e-37;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVDIK 108


RESULT 8
US-10-041-860-47
; Sequence 47, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-47

  Query Match             95.5%;  Score 531;  DB 14;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 2.6e-37;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK 108


RESULT 9
US-10-041-860-226
; Sequence 226, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
```

```
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 226
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-226

  Query Match             95.5%;  Score 531;  DB 14;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 2.6e-37;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK 108


RESULT 10
US-10-041-860-260
; Sequence 260, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 260
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-260

  Query Match             95.5%;  Score 531;  DB 14;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 2.6e-37;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK 108


RESULT 11
US-10-041-860-369
; Sequence 369, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 369
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-369

  Query Match             95.5%;  Score 531;  DB 14;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 2.6e-37;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK 108


RESULT 12
US-10-665-383-72
; Sequence 72, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
;  APPLICANT: Floege, Juergen
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Keyt, Bruce
;  APPLICANT:  LaRochelle, William
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
;  TITLE OF INVENTION:  USING ANTI-PDGF-DD ANTIBODIES
;  FILE REFERENCE: ABGENIX.052A
;  CURRENT APPLICATION NUMBER: US/10/665,383
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: 60/411,137
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-665-383-72

  Query Match             95.5%;  Score 531;  DB 16;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 2.6e-37;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK 108


RESULT 13
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US-10-726-332-213
; Sequence 213, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 213
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-213

  Query Match             94.3%;  Score 524.5;  DB 17;  Length 110;
  Best Local Similarity   95.4%;  Pred. No. 9.2e-37;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||: | |  ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109


RESULT 14
US-09-453-234-52
; Sequence 52, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-25L
US-09-453-234-52

  Query Match             94.3%;  Score 524.5;  DB 10;  Length 224;
  Best Local Similarity   96.3%;  Pred. No. 1.8e-36;
  Matches  104;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              :|||||||||||||||||||||||||||||:  ||||||||||||||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIK 107


RESULT 15
US-10-706-689-39
; Sequence 39, Application US/10706689
; Publication No. US20050100965A1
; GENERAL INFORMATION:
;  APPLICANT: Ghayur, Tariq
;  APPLICANT:  Labkovsky, Boris
;  APPLICANT:  Voss, Jeffrey
;  APPLICANT:  Green, Larry
;  APPLICANT:  Babcook, John
;  APPLICANT:  Jia, Xiao-chi
;  APPLICANT:  Wieler, James
;  APPLICANT:  Kang, Paul
;  APPLICANT:  Hegberg, Brad
;  TITLE OF INVENTION: IL-18 Binding Proteins
;  FILE REFERENCE: BBC-085
;  CURRENT APPLICATION NUMBER: US/10/706,689
;  CURRENT FILING DATE:  2003-11-12
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 39
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-706-689-39

  Query Match             94.2%;  Score 524;  DB 17;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 1e-36;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||:|||||||||||||||||||||:|||||||||| ||||||||||||||||||||
Db          1 EILLTQSPGTLSLSPGERATLSCRASQNVSSSYLAWYQQNPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||| |||||:|| | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFEVYYCQQSGSSLFTFGPGTKVDIK 108


Search completed: August 18, 2005, 07:08:03
Job time : 205.676 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 43.1237 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-8
Perfect score: 556
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQRSGGSSFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	517	93.0	109	2	H30601	Ig kappa chain V-I
2	517	93.0	109	2	B30601	Ig kappa chain V-I
3	515	92.6	108	2	C30608	Ig kappa chain V-I
4	514	92.4	109	2	A30608	Ig kappa chain V-I
5	514	92.4	109	2	C30601	Ig kappa chain V-I
6	514	92.4	109	2	D30601	Ig kappa chain V-I
7	512	92.1	109	2	G30607	Ig kappa chain V-I
8	512	92.1	129	1	K3HUHA	Ig kappa chain pre
9	512	92.1	129	1	K3HUHI	Ig kappa chain pre
10	511	91.9	107	2	PH0965	Ig kappa chain V r
11	511	91.9	129	2	S46369	IG light chain var
12	511	91.9	134	2	S38643	Ig kappa chain V r
13	510	91.7	109	2	F30607	Ig kappa chain V-I
14	508	91.4	109	2	PH0963	Ig kappa chain V r
15	506	91.0	109	2	G30601	Ig kappa chain V-I
16	506	91.0	129	2	S49532	anti-Sm antibody V
17	505.5	90.9	114	2	S46375	Ig kappa chain V-J
18	504	90.6	109	1	K3HUSI	Ig kappa chain V-I
19	503	90.5	109	2	F30601	Ig kappa chain V-I
20	503	90.5	128	2	S20636	Ig kappa chain V r
21	501	90.1	109	1	K3HUWL	Ig kappa chain V-I
22	499	89.7	124	2	S20633	Ig kappa chain - h
23	497.5	89.5	129	2	S40325	Ig kappa chain - h
24	497	89.4	108	2	B30608	Ig kappa chain V-I
25	497	89.4	109	1	K3HUTI	Ig kappa chain V-I
26	496.5	89.3	110	2	E30607	Ig kappa chain V-I
27	495	89.0	121	2	S40327	Ig kappa chain - h
28	493	88.7	110	2	S20635	Ig kappa chain V r
29	493	88.7	130	2	S20637	Ig kappa chain V r
30	491.5	88.4	108	2	H44151	Ig kappa chain V r
31	491.5	88.4	110	2	S44120	Ig kappa chain V-J
32	488.5	87.9	104	2	PH0964	Ig kappa chain V r
33	484	87.1	108	1	K3HUB6	Ig kappa chain V-I
34	484	87.1	109	2	F44151	Ig kappa chain V r
35	482.5	86.8	108	2	E30609	Ig kappa chain V-I
36	482	86.7	129	2	A32274	Ig kappa chain pre
37	480	86.3	108	2	S33988	Ig kappa chain V r
38	476	85.6	109	1	K3HUGO	Ig kappa chain V-I
39	474	85.3	127	2	S40380	Ig kappa chain V-J
40	473	85.1	109	2	S47181	Ig kappa chain - h
41	472	84.9	215	2	JE0242	Ig kappa chain NIG
42	471	84.7	96	2	A30601	Ig kappa chain V-I
43	471	84.7	116	2	B27594	Ig kappa chain pre
44	469	84.4	215	2	A23746	Ig kappa chain V-I
45	468	84.2	116	2	C27594	Ig kappa chain pre

ALIGNMENTS

RESULT 1
H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: H30601; E30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON1>
A;Accession: E30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 517; DB 2; Length 109;
Best Local Similarity 92.6%; Pred. No. 3.6e-36;
Matches 100; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||: | | :||| |||::||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPYTFGQGTKLEIK 108
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RESULT 2
B30601
Ig kappa chain V-III region (Glo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: B30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: B30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

```
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             93.0%;  Score 517;  DB 2;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 3.6e-36;
  Matches  101;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||: | |  ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK 108


RESULT 3
C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: C30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: C30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-108 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             92.6%;  Score 515;  DB 2;  Length 108;
  Best Local Similarity   92.6%;  Pred. No. 5.2e-36;
  Matches  100;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||: | |  :||| ||||::||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKLEIK 108


RESULT 4
A30608
Ig kappa chain V-III region (Son) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: A30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: A30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             92.4%;  Score 514;  DB 2;  Length 109;
  Best Local Similarity   92.6%;  Pred. No. 6.4e-36;
  Matches  100;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              :||||||||||||||||||||||||||||: | |  :||| ||||:||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPYTFGGGTKVEIK 108


RESULT 5
C30601
Ig kappa chain V-III region (Pay) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: C30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: C30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             92.4%;  Score 514;  DB 2;  Length 109;
  Best Local Similarity   92.6%;  Pred. No. 6.4e-36;
  Matches  100;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||: | |  ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK 108


RESULT 6
D30601
Ig kappa chain V-III region (Cur) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: D30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: D30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             92.4%;  Score 514;  DB 2;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 6.4e-36;
  Matches  101;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||: | |  ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIK 108


RESULT 7
G30607
Ig kappa chain V-III region (Kas) - human (fragment)
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C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: G30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: G30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             92.1%;  Score 512;  DB 2;  Length 109;
  Best Local Similarity   90.7%;  Pred. No. 9.3e-36;
  Matches   98;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              :|||||||||||||||||||||||||||:||:|||||||||||||||||||||||||:|
Db          1 DIVLTQSPGTLSLSPGERATLSCRASQSLSSTYLAWYQQKPGQAPRLLIYGASSRATGVP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||: | | |||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIK 108


RESULT 8
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: PL0022
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A;Reference number: PL0021; MUID:88171307; PMID:3127527
A;Accession: PL0022
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
A;Cross-references: UNIPROT:P18135
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F;21-117/Region: V segment
F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;118-129/Region: J segment (JK1)
F;43-109/Disulfide bonds: #status predicted

  Query Match             92.1%;  Score 512;  DB 1;  Length 129;
  Best Local Similarity   93.5%;  Pred. No. 1.1e-35;
  Matches  101;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | |  ||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPRTFGQGTKVEIK 128


RESULT 9
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: PL0021
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A;Reference number: PL0021; MUID:88171307; PMID:3127527
A;Accession: PL0021
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
A;Cross-references: UNIPROT:P18136
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F;21-117/Region: V segment
F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;118-129/Region: J segment (JK1)
F;43-109/Disulfide bonds: #status predicted

  Query Match             92.1%;  Score 512;  DB 1;  Length 129;
  Best Local Similarity   92.6%;  Pred. No. 1.1e-35;
  Matches  100;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||| |||||||: | | :||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLEPXDFAVYYCQQYGSSPWTFGQGTKVEIK 128


RESULT 10
PH0965
Ig kappa chain V region (G6+ CLL-BRA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PH0965
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0965
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-107 <MAR>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-21/Region: framework 1
F;14-89/Domain: immunoglobulin homology <IMM>
F;22-32/Region: complementarity-determining 1
F;33-48/Region: framework 2
F;49-54/Region: complementarity-determining 2
F;55-87/Region: framework 3
F;88-95/Region: complementarity-determining 3

  Query Match             91.9%;  Score 511;  DB 2;  Length 107;
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  Best Local Similarity   93.4%;  Pred. No. 1.1e-35;
  Matches   99;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 VLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDR 60

Qy         63 FSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | | :||| ||||:||
Db         61 FSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSRYTFGQGTKVEIK 106


RESULT 11
S46369
IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S46369
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46369
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <BEN>
A;Cross-references: EMBL:Z27170
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>

  Query Match             91.9%;  Score 511;  DB 2;  Length 129;
  Best Local Similarity   91.7%;  Pred. No. 1.3e-35;
  Matches   99;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | | | || ||:::||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFPFGQGTRLEIK 128


RESULT 12
S38643
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38643
R;Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <BEN>
A;Cross-references: EMBL:Z27170; NID:g415955; PIDN:CAA81694.1; PID:g415956
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-116/Domain: immunoglobulin homology <IMM>

  Query Match             91.9%;  Score 511;  DB 2;  Length 134;
  Best Local Similarity   91.7%;  Pred. No. 1.4e-35;
  Matches   99;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 85

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | | | || ||:::||
Db         86 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFPFGQGTRLEIK 133


RESULT 13
F30607
Ig kappa chain V-III region (Bor) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: F30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: F30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             91.7%;  Score 510;  DB 2;  Length 109;
  Best Local Similarity   92.6%;  Pred. No. 1.4e-35;
  Matches  100;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||| |||||: | |  ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFVVYYCQQYGNSPQTFGQGTKVEIK 108


RESULT 14
PH0963
Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PH0963
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0963
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-109 <MAR>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-91/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-50/Region: framework 2
F;51-56/Region: complementarity-determining 2
F;57-89/Region: framework 3
F;90-97/Region: complementarity-determining 3

  Query Match             91.4%;  Score 508;  DB 2;  Length 109;
  Best Local Similarity   92.6%;  Pred. No. 2e-35;
  Matches  100;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | |   || ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPAFGQGTKVEIK 108
```

RESULT 15
G30601
Ig kappa chain V-III region (Got) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: G30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: G30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 91.0%; Score 506; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 2.9e-35;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||: | |  ||| |||::||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKLEIK 108
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Search completed: August 18, 2005, 06:20:07
Job time : 43.1237 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 46.7173 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-6
Perfect score: 623
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SGSYFYFDLWGRGTLVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	570	91.5	123	2	C36006	Ig heavy chain V r
2	567	91.0	123	2	S38492	Ig heavy chain - h
3	561.5	90.1	139	2	PH1558	Ig heavy chain V r
4	550.5	88.4	136	2	A49047	Ig heavy chain V r
5	550	88.3	113	2	PH1428	Ig heavy chain V r
6	546.5	87.7	134	2	PH1422	Ig heavy chain V r
7	536	86.0	127	2	PH1414	Ig heavy chain V r
8	533	85.6	127	2	PH1420	Ig heavy chain V r
9	532	85.4	136	2	PH1559	Ig heavy chain V r
10	530	85.1	125	2	PH1410	Ig heavy chain V r
11	527	84.6	123	2	PH1423	Ig heavy chain V r
12	526.5	84.5	126	2	PH1424	Ig heavy chain V r
13	525.5	84.3	126	2	PH1419	Ig heavy chain V r
14	524	84.1	127	2	PH1415	Ig heavy chain V r
15	519.5	83.4	126	2	PH1417	Ig heavy chain V r
16	519.5	83.4	126	2	PH1418	Ig heavy chain V r
17	515.5	82.7	126	2	PH1416	Ig heavy chain V r
18	509	81.7	117	2	S19670	Ig heavy chain V r
19	505	81.1	123	2	PH1413	Ig heavy chain V r
20	504.5	81.0	147	2	PH1561	Ig heavy chain V r
21	504	80.9	138	2	PH1565	Ig heavy chain V r
22	504	80.9	144	2	PH1563	Ig heavy chain V r
23	502	80.6	109	2	PH1672	Ig heavy chain V r
24	498.5	80.0	137	2	PH1562	Ig heavy chain V r
25	498	79.9	98	2	S26907	Ig heavy chain V r
26	498	79.9	101	2	S12424	Ig heavy chain V r
27	498	79.9	102	2	PH1266	Ig heavy chain V r
28	498	79.9	102	2	PH1279	Ig heavy chain V r
29	498	79.9	115	2	PH1557	Ig heavy chain V r
30	498	79.9	128	2	S16685	Ig heavy chain V r
31	496.5	79.7	122	2	PC4280	anti-SS-A/Ro 60K p
32	496.5	79.7	141	2	S31685	Ig heavy chain V r
33	496	79.6	144	2	E41287	Ig heavy chain pre
34	495	79.5	102	2	PH1252	Ig heavy chain V r
35	495	79.5	117	2	S19669	Ig heavy chain V r
36	494	79.3	127	2	PH1411	Ig heavy chain V r
37	493	79.1	101	2	S12428	Ig heavy chain V r
38	493	79.1	117	2	A28846	Ig heavy chain pre
39	492	79.0	102	2	PH1281	Ig heavy chain V r
40	492	79.0	102	2	PH1271	Ig heavy chain V r
41	492	79.0	102	2	PH1278	Ig heavy chain V r
42	490.5	78.7	122	2	PC4279	anti-SS-A/Ro 60K p
43	490	78.7	102	2	PH1273	Ig heavy chain V r
44	490	78.7	102	2	PH1254	Ig heavy chain V r
45	489	78.5	102	2	PH1258	Ig heavy chain V r

ALIGNMENTS

RESULT 1
C36006
Ig heavy chain V region (83p2) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: C36006
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36006
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <SCH>
A;Cross-references: GB:M34022
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 91.5%; Score 570; DB 2; Length 123;
Best Local Similarity 89.4%; Pred. No. 3.8e-46;
Matches 110; Conservative 2; Mismatches 5; Indels 6; Gaps 1;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG------SGSYFYFDLWGRGTLVT 114
              |||||||||||||||||||||||||||||||||||         | :||||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHNSQTGASLWYFDLWGRGTLVT 120

Qy        115 VSS 117
              |||
Db        121 VSS 123
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RESULT 2
S38492
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38492
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a p
A;Reference number: S38488
A;Accession: S38492
A;Status: preliminary

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A;Molecule type: DNA
A;Residues: 1-123 <MAR>
A;Cross-references: EMBL:Z23034; NID:g414031; PIDN:CAA80569.1; PID:g414032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             91.0%;  Score 567;  DB 2;  Length 123;
  Best Local Similarity   88.6%;  Pred. No. 7.2e-46;
  Matches  109;  Conservative    3;  Mismatches    5;  Indels    6;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY------FYFDLWGRGTLVT 114
              |||||||||||||||||||||||||||||||||||     |      :|||||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARRRYSYAQHDWYFDLWGRGTLVT 120

Qy        115 VSS 117
              |||
Db        121 VSS 123


RESULT 3
PH1558
Ig heavy chain V region (clone DOB) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
C;Accession: PH1558
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymp
A;Reference number: PH1557; MUID:93210459; PMID:7681468
A;Accession: PH1558
A;Molecule type: DNA
A;Residues: 1-139 <RAS>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>

  Query Match             90.1%;  Score 561.5;  DB 2;  Length 139;
  Best Local Similarity   89.3%;  Pred. No. 2.7e-45;
  Matches  109;  Conservative    2;  Mismatches    6;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db         18 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 77

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC-----GSGSYFYFDLWGRGTLVTV 115
              |||||||||||||||||||||||||||||||||||      || |  || ||:||||||
Db         78 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARSISSSGYYSNFDYWGQGTLVTV 137

Qy        116 SS 117
              ||
Db        138 SS 139


RESULT 4
A49047
Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (fr
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C;Accession: A49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: A49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-136 <VIC>
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113206, NCBIP:113207)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             88.4%;  Score 550.5;  DB 2;  Length 136;
  Best Local Similarity   81.1%;  Pred. No. 2.8e-44;
  Matches  107;  Conservative    3;  Mismatches    7;  Indels   15;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          5 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 64

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYF---------------D 105
              |||||||||||||||||||||||||||||||||||||||||||   || |:               |
Db         65 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQSYGYYDFRSGYYPAYYYYGMD 124

Qy        106 LWGRGTLVTVSS 117
              :|| || |||||
Db        125 VWGEGTTVTVSS 136


RESULT 5
PH1428
Ig heavy chain V region (clone VH5-1R1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999
C;Accession: PH1428
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sh
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1428
A;Molecule type: mRNA
A;Residues: 1-113 <VAN>
A;Cross-references: GB:S51905; NID:g262690; PIDN:AAC80261.1; PID:g262691
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.3%;  Score 550;  DB 2;  Length 113;
  Best Local Similarity   89.7%;  Pred. No. 2.5e-44;
  Matches  105;  Conservative    4;  Mismatches    4;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||||||||||       ||:||:||:|||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARA----FDVWGQGTMVTVSS 113


RESULT 6
PH1422
Ig heavy chain V region (clone P3-69) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1422
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sh
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1422
A;Molecule type: mRNA
A;Residues: 1-134 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon ATG for residue 93 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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  Query Match             87.7%;  Score 546.5;  DB 2;  Length 134;
  Best Local Similarity   81.5%;  Pred. No. 6.4e-44;
  Matches  106;  Conservative    5;  Mismatches    6;  Indels   13;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:| :||| |||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFITYWIAWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---------GSGS----YFYFDLW 107
              |||||||||| ||||||||||||||||||||||||         ||||    |:| |:|
Db         61 SPSFQGQVTISVDKSISTAYLQWSSLKASDTAMYYCARHGMEYYYGSGSSDYYYYYMDVW 120

Qy        108 GRGTLVTVSS 117
              |:|| |||||
Db        121 GKGTTVTVSS 130


RESULT 7
PH1414
Ig heavy chain V region (clone P1-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1414
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1414
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon TTG for residue 119 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.0%;  Score 536;  DB 2;  Length 127;
  Best Local Similarity   84.6%;  Pred. No. 5.7e-43;
  Matches  104;  Conservative    5;  Mismatches    8;  Indels    6;  Gaps    1;

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Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY------FYFDLWGRGTLVT 114
              |||||||||||:|||||||||||||:|||||||    |         || ||:|||||
Db         61 SPSFQGQVTISADESISTAYLQWSSLKATDTAMYYCARRDYGDYQSTGGFDPWGQGTLVT 120

Qy        115 VSS 117
              |||
Db        121 VSS 123


RESULT 8
PH1420
Ig heavy chain V region (clone P2-55) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1420
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1420
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon CTT for residue 101 as Phe
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

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  Best Local Similarity   82.9%;  Pred. No. 1.1e-42;
  Matches  102;  Conservative    7;  Mismatches    8;  Indels    6;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:||:|||||||:|||||| |||||| ||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWIGWVRQVPGKGLEWMGIIYPADSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC------GSGSYFYFDLWGRGTLVT 114
              |||||||||||||||||||||||:|||||:|||      |:    :|| ||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLRASDTAIYYCARHGLHGTSFSSWFDFWGRGTLVT 120

Qy        115 VSS 117
              | |
Db        121 VPS 123


RESULT 9
PH1559
Ig heavy chain V region (clone HAN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PH1559
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymp
A;Reference number: PH1557; MUID:93210459; PMID:7681468
A;Accession: PH1559
A;Molecule type: DNA
A;Residues: 1-136 <RAS>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>

  Query Match             85.4%;  Score 532;  DB 2;  Length 136;
  Best Local Similarity   86.6%;  Pred. No. 1.5e-42;
  Matches  103;  Conservative    3;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||| |:|||||||||||||||| ||||||||||||
Db         18 EVQLVQSGAEVKKPGESLKISCKGSRYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 77

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGS--GSYFYFDLWGRGTLVTVSS 117
              ||||||||| |||||||||||||| ||||||||||    | :   | ||:|||||||
Db         78 SPSFQGQVTFSADKSISTAYLQWSRLKASDTAMYYCARLYGDFSTVDYWGQGTLVTVSS 136


RESULT 10
PH1410
Ig heavy chain V region (clone P1-52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1410
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1410
A;Molecule type: mRNA
A;Residues: 1-125 <VAN>
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             85.1%;  Score 530;  DB 2;  Length 125;
  Best Local Similarity   82.6%;  Pred. No. 2e-42;
  Matches  100;  Conservative    7;  Mismatches   10;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||:|||||||||| :||| |||||||||| :||||| ||| ||
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Db          1 EVQLVQSGAEVKKPGESLQISCKGSGYNFNTYWIAWVRQMPGKGLEYIGIIYPDDSDIRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYFYFDLWGRGTLVTVS 116
               |||||||||||||||||||||||| ||||||||:||    |  |:| || ||:||:|||| 
Db         61 SPSFQGQVTISADKSISTAYLQWSGLKASDTAMFYCARLKGENSHFLFDFWGQGTMVTVS 120

Qy        117 S 117
               |
Db        121 S 121


RESULT 11
PH1423
Ig heavy chain V region (clone P3-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1423
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1423
A;Molecule type: mRNA
A;Residues: 1-123 <VAN>
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.6%;  Score 527;  DB 2;  Length 123;
  Best Local Similarity   84.0%;  Pred. No. 3.8e-42;
  Matches  100;  Conservative    9;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:| :||| |||||||||||| ||||||||||||| 
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFITYWIAWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCG--SGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||:|||   : :: :| :||:|||| ||| 
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAIYYCARHADNFDWFQIWGQGTLVIVSS 119


RESULT 12
PH1424
Ig heavy chain V region (clone P3-60) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1424
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1424
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.5%;  Score 526.5;  DB 2;  Length 126;
  Best Local Similarity   82.8%;  Pred. No. 4.4e-42;
  Matches  101;  Conservative    6;  Mismatches   10;  Indels    5;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              | |||||||||||||||||||:|||| ||: |||||||||||||| |||||||||| || 
Db          1 EEQLVQSGAEVKKPGESLKISCQGSGYRFTNSWIGWVRQMPGKGLEWMGIIYPGDSDIRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC-----GSGSYFYFDLWGRGTLVTV 115
              ||:|||||||| |||||||||||||||||||||||     |  :| || :||:|||||| 
Db         61 SPAFQGQVTISVDKSISTAYLQWSSLKASDTAMYYCARTHRGGTNYEYFQVWGQGTLVTV 120

Qy        116 SS 117
               ||
Db        121 SS 122


RESULT 13
PH1419
Ig heavy chain V region (clone P2-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1419
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sl
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1419
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon ACT for residue 107 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.3%;  Score 525.5;  DB 2;  Length 126;
  Best Local Similarity   80.3%;  Pred. No. 5.4e-42;
  Matches   98;  Conservative   15;  Mismatches    4;  Indels    5;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||| :|||||||||||||||::||:||||||||||:||| :|||||| |||||| 
Db          1 EVQLVQSGEDVKKPGESLKISCKGSGFSFTNYWIGWVRQMPGEGLEWVGIIYPDDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYFY-FDLWGRGTLVTV 115
              |||||||:||||||||:|||||||:|||||:|||||    |||:|:  ||:||:||:||| 
Db         61 SPSFQGQITISADKSINTAYLQWSNLKASDSAMYYCARPRGSGTYYTGFDIWGQGTMVTV 120

Qy        116 SS 117
               ||
Db        121 SS 122


RESULT 14
PH1415
Ig heavy chain V region (clone P1-57) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1415
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sl
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1415
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon TTG for residue 118 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.1%;  Score 524;  DB 2;  Length 127;
  Best Local Similarity   83.7%;  Pred. No. 7.5e-42;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWIGWVRQMPGKGLEWMVIIYPGDSDIRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCGSGSY------FYFDLWGRGTLVT 114
              |||||||||||||:|||||||||||||||||||||    |        || ||:||||| 
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Db         61 SPSFQGQVTISADESISTAYLQWSSLKASDTAMYYCARRDYGDYQSTGGFDPWGQGTLVT 120

Qy        115 VSS 117
              |||
Db        121 VSS 123
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RESULT 15
PH1417
Ig heavy chain V region (clone P2-52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C;Accession: PH1417
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1417
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Experimental source: PBMC
A;Note: the authors translated the codon ATC for residue 111 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match   83.4%; Score 519.5; DB 2; Length 126;
  Best Local Similarity   80.3%; Pred. No. 2e-41;
  Matches   98; Conservative   13; Mismatches   6; Indels   5; Gaps   2;

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Db          1 EVQLVQSGEEVKKPGESLKITCKGPGFSFTNYWIGWVRQMPGKGLEWVGIIYPDDSDARY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC----GSGSYFY-FDLWGRGTLVTV 115
              |||||||||||||||:||||||||:|||:|||||    |||:|:  ||:||:||:|||
Db         61 SPSFQGQVTISADKSISSAYLQWSSLRASDSAMYYCARPRGSGTYYTGFDIWGQGTMVTV 120

Qy        116 SS 117
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Db        121 SS 122
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Job time : 47.7173 secs

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OM protein - protein search, using sw model

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Perfect score: 623
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SGSYFYFDLWGRGTLVTVSS 117

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	567	91.0	119	3	US-09-025-769B-26	Sequence 26, Appl
2	567	91.0	119	4	US-09-490-070A-26	Sequence 26, Appl
3	567	91.0	119	4	US-09-490-153-26	Sequence 26, Appl
4	567	91.0	119	4	US-09-490-324-26	Sequence 26, Appl
5	554.5	89.0	120	3	US-09-025-769B-40	Sequence 40, Appl
6	554.5	89.0	120	3	US-09-025-769B-67	Sequence 67, Appl
7	554.5	89.0	120	4	US-09-490-070A-40	Sequence 40, Appl
8	554.5	89.0	120	4	US-09-490-070A-67	Sequence 67, Appl
9	554.5	89.0	120	4	US-09-490-153-40	Sequence 40, Appl
10	554.5	89.0	120	4	US-09-490-153-67	Sequence 67, Appl
11	554.5	89.0	120	4	US-09-490-324-40	Sequence 40, Appl
12	554.5	89.0	120	4	US-09-490-324-67	Sequence 67, Appl
13	500	80.3	129	2	US-08-665-202-32	Sequence 32, Appl
14	500	80.3	129	4	US-09-315-574-32	Sequence 32, Appl
15	500	80.3	258	2	US-08-665-202-5	Sequence 5, Appli
16	500	80.3	258	4	US-09-315-574-5	Sequence 5, Appli
17	500	80.3	262	3	US-09-069-821-4	Sequence 4, Appli
18	500	80.3	262	4	US-09-956-086-4	Sequence 4, Appli
19	500	80.3	262	4	US-09-956-087-4	Sequence 4, Appli
20	500	80.3	282	3	US-09-420-592A-7	Sequence 7, Appli
21	500	80.3	282	4	US-09-985-442-7	Sequence 7, Appli
22	500	80.3	282	4	US-09-983-580-7	Sequence 7, Appli
23	498	79.9	98	2	US-08-665-202-33	Sequence 33, Appl
24	498	79.9	98	4	US-09-315-574-33	Sequence 33, Appl
25	498	79.9	117	3	US-08-545-809A-133	Sequence 133, App
26	493	79.1	98	1	US-08-478-039-81	Sequence 81, Appl
27	493	79.1	98	1	US-08-476-349A-81	Sequence 81, Appl
28	484	77.7	111	4	US-09-726-219A-171	Sequence 171, App
29	483	77.5	125	2	US-08-665-202-44	Sequence 44, Appl
30	483	77.5	125	2	US-08-665-202-53	Sequence 53, Appl
31	483	77.5	125	2	US-08-665-202-54	Sequence 54, Appl
32	483	77.5	125	4	US-09-315-574-44	Sequence 44, Appl
33	483	77.5	125	4	US-09-315-574-53	Sequence 53, Appl
34	483	77.5	125	4	US-09-315-574-54	Sequence 54, Appl
35	481	77.2	125	2	US-08-665-202-45	Sequence 45, Appl
36	481	77.2	125	2	US-08-665-202-46	Sequence 46, Appl
37	481	77.2	125	2	US-08-665-202-48	Sequence 48, Appl
38	481	77.2	125	2	US-08-665-202-55	Sequence 55, Appl
39	481	77.2	125	4	US-09-315-574-45	Sequence 45, Appl
40	481	77.2	125	4	US-09-315-574-46	Sequence 46, Appl
41	481	77.2	125	4	US-09-315-574-48	Sequence 48, Appl
42	481	77.2	125	4	US-09-315-574-55	Sequence 55, Appl
43	478	76.7	125	2	US-08-665-202-51	Sequence 51, Appl
44	478	76.7	125	2	US-08-665-202-52	Sequence 52, Appl
45	478	76.7	125	4	US-09-315-574-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-26

Query Match 91.0%; Score 567; DB 3; Length 119;
Best Local Similarity 91.7%; Pred. No. 4.7e-52;
Matches 110; Conservative 2; Mismatches 4; Indels 4; Gaps 2;

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Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||    | | | ||| ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGGGGY-YFDYWGQGTLVTVSS 119


RESULT 2
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

  Query Match             91.0%;  Score 567;  DB 4;  Length 119;
  Best Local Similarity   91.7%;  Pred. No. 4.7e-52;
  Matches  110;  Conservative    2;  Mismatches    4;  Indels    4;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
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Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGGGGY-YFDYWGQGTLVTVSS 119


RESULT 3
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10021
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,153
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/025,769B
;             FILING DATE: 18-FEB-1998
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: James F. Haley, Jr., Esq.
;             REGISTRATION NUMBER: 27,794
;             REFERENCE/DOCKET NUMBER: MORPHO/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)596-9000
;             TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

  Query Match             91.0%;  Score 567;  DB 4;  Length 119;
  Best Local Similarity   91.7%;  Pred. No. 4.7e-52;
  Matches  110;  Conservative    2;  Mismatches    4;  Indels    4;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
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Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
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Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGGGGY-YFDYWGQGTLVTVSS 119


RESULT 4
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
```

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;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,324
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

  Query Match             91.0%;  Score 567;  DB 4;  Length 119;
  Best Local Similarity   91.7%;  Pred. No. 4.7e-52;
  Matches  110;  Conservative    2;  Mismatches    4;  Indels    4;  Gaps    2;

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              ||||||||||||||||||||||||||||:||||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||    | | | ||| ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLGGGGY-YFDYWGQGTLVTVSS 119


RESULT 5
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-40

  Query Match             89.0%;  Score 554.5;  DB 3;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||||:|||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||    |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 6
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
```

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;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-67

  Query Match             89.0%;  Score 554.5;  DB 3;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||   |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 7
US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

  Query Match             89.0%;  Score 554.5;  DB 4;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||   |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 8
US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 67:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

  Query Match             89.0%;  Score 554.5;  DB 4;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              |||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||   |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120
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```
RESULT 9
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10021
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,153
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/025,769B
;             FILING DATE: 18-FEB-1998
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: James F. Haley, Jr., Esq.
;             REGISTRATION NUMBER: 27,794
;             REFERENCE/DOCKET NUMBER: MORPHO/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)596-9000
;             TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

  Query Match             89.0%;  Score 554.5;  DB 4;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||    |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 10
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10021
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,153
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/025,769B
;             FILING DATE: 18-FEB-1998
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: James F. Haley, Jr., Esq.
;             REGISTRATION NUMBER: 27,794
;             REFERENCE/DOCKET NUMBER: MORPHO/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)596-9000
;             TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 67:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

  Query Match             89.0%;  Score 554.5;  DB 4;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||    |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 11
US-09-490-324-40
; Sequence 40, Application US/09490324
; Patent No. 6828422
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
```

```
;           ZIP: 10021
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/490,324
;           FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/025,769
;           FILING DATE: 18-FEB-1998
;           APPLICATION NUMBER: EP 95 11 3021.0
;           FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;           NAME: James F. Haley, Jr., Esq.
;           REGISTRATION NUMBER: 27,794
;           REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212)596-9000
;           TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 40:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 120 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-324-40

  Query Match             89.0%;  Score 554.5;  DB 4;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||    |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 12
US-09-490-324-67
; Sequence 67, Application US/09490324
; Patent No. 6828422
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;           STREET: 1251 Avenue of the Americas
;           CITY: New York
;           STATE: New York
;           COUNTRY: USA
;           ZIP: 10021
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/490,324
;           FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/025,769
;           FILING DATE: 18-FEB-1998
;           APPLICATION NUMBER: EP 95 11 3021.0
;           FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;           NAME: James F. Haley, Jr., Esq.
;           REGISTRATION NUMBER: 27,794
;           REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212)596-9000
;           TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 67:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 120 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-324-67

  Query Match             89.0%;  Score 554.5;  DB 4;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 9.7e-51;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              ||||||||||||||||||||||||||:||||||||||||||||| ||||||||||||
Db          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC---GSGSYFYFDLWGRGTLVTVSS 117
              |||||||||||||||||||||||||||||||||||    |   ::  | ||:||||||||
Db         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARWGGDGFYAMDYWGQGTLVTVSS 120


RESULT 13
US-08-665-202-32
; Sequence 32, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  32:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-32

  Query Match             80.3%;  Score 500;  DB 2;  Length 129;
  Best Local Similarity   74.4%;  Pred. No. 5.5e-45;
  Matches   96;  Conservative   11;  Mismatches   10;  Indels   12;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||:|||||:||||||||||||||||:|||||| |||||||||| ||:|||||||:|
Db          1 QVQLLQSGAELKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEYMGLIYPGDSDTKY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMY--------YCGSGSYF----YFDLWG 108
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Db         61 SPSFQGQVTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKWPEYFQHWG 120

Qy        109 RGTLVTVSS 117
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Db        121 QGTLVTVSS 129


RESULT 14
US-09-315-574-32
; Sequence 32, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/315,574
;      FILING DATE:  20-MAY-99
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,202
;      FILING DATE:  13-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-315-574-32

  Query Match             80.3%;  Score 500;  DB 4;  Length 129;
  Best Local Similarity   74.4%;  Pred. No. 5.5e-45;
  Matches   96;  Conservative   11;  Mismatches   10;  Indels   12;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
              :|||:|||||:||||||||||||||||:|||||| |||||||||| ||:|||||||:|
Db          1 QVQLLQSGAELKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEYMGLIYPGDSDTKY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMY--------YCGSGSYF----YFDLWG 108
              |||||||||| |||:|||||||||| ||:|:|        || | :      ||  ||
Db         61 SPSFQGQVTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKWPEYFQHWG 120

Qy        109 RGTLVTVSS 117
              :|||||||
Db        121 QGTLVTVSS 129


RESULT 15
US-08-665-202-5
; Sequence 5, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  258 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-665-202-5

  Query Match             80.3%;  Score 500;  DB 2;  Length 258;
  Best Local Similarity   74.4%;  Pred. No. 1.2e-44;
  Matches   96;  Conservative   11;  Mismatches   10;  Indels   12;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGESLKISCKGSGYNFTSYWIGWVRQMPGKGLELMGIIYPGDSDTRY 60
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Db          1 QVQLLQSGAELKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEYMGLIYPGDSDTKY 60

Qy         61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMY--------YCGSGSYF----YFDLWG 108
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Db         61 SPSFQGQVTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKWPEYFQHWG 120

Qy        109 RGTLVTVSS 117
              :|||||||
Db        121 QGTLVTVSS 129


Search completed: August 18, 2005, 06:22:52
Job time : 66.735 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 60.6784 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-8
Perfect score: 556
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQRSGGSSFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	524.5	94.3	224	4	US-09-456-090A-52	Sequence 52, Appl
2	524.5	94.3	224	4	US-09-453-234-52	Sequence 52, Appl
3	522.5	94.0	226	4	US-09-456-090A-42	Sequence 42, Appl
4	522.5	94.0	226	4	US-09-453-234-42	Sequence 42, Appl
5	520	93.5	109	3	US-09-025-769B-16	Sequence 16, Appl
6	520	93.5	109	4	US-09-490-070A-16	Sequence 16, Appl
7	520	93.5	109	4	US-09-490-153-16	Sequence 16, Appl
8	520	93.5	109	4	US-09-490-324-16	Sequence 16, Appl
9	518.5	93.3	224	4	US-09-456-090A-76	Sequence 76, Appl
10	518.5	93.3	224	4	US-09-453-234-76	Sequence 76, Appl
11	518.5	93.3	226	4	US-09-456-090A-72	Sequence 72, Appl
12	518.5	93.3	226	4	US-09-453-234-72	Sequence 72, Appl
13	517.5	93.1	224	4	US-09-456-090A-40	Sequence 40, Appl
14	517.5	93.1	224	4	US-09-453-234-40	Sequence 40, Appl
15	516.5	92.9	226	4	US-09-456-090A-38	Sequence 38, Appl
16	516.5	92.9	226	4	US-09-453-234-38	Sequence 38, Appl
17	515.5	92.7	224	4	US-09-456-090A-44	Sequence 44, Appl
18	515.5	92.7	224	4	US-09-456-090A-78	Sequence 78, Appl
19	515.5	92.7	224	4	US-09-453-234-44	Sequence 44, Appl
20	515.5	92.7	224	4	US-09-453-234-78	Sequence 78, Appl
21	514	92.4	108	2	US-08-232-081B-42	Sequence 42, Appl
22	509	91.5	108	1	US-08-488-113B-150	Sequence 150, App
23	509	91.5	108	1	US-08-477-484B-150	Sequence 150, App
24	509	91.5	108	2	US-08-646-360-150	Sequence 150, App
25	509	91.5	108	3	US-08-839-765-150	Sequence 150, App
26	509	91.5	108	3	US-09-136-389-150	Sequence 150, App
27	509	91.5	108	3	US-09-610-838-150	Sequence 150, App
28	509	91.5	108	4	US-09-711-485-150	Sequence 150, App
29	508	91.4	235	4	US-09-472-087-14	Sequence 14, Appl
30	508	91.4	235	4	US-09-472-087-65	Sequence 65, Appl
31	506.5	91.1	226	4	US-09-456-090A-50	Sequence 50, Appl
32	506.5	91.1	226	4	US-09-456-090A-86	Sequence 86, Appl
33	506.5	91.1	226	4	US-09-453-234-50	Sequence 50, Appl
34	506.5	91.1	226	4	US-09-453-234-86	Sequence 86, Appl
35	505.5	90.9	234	4	US-09-472-087-17	Sequence 17, Appl
36	505.5	90.9	234	4	US-09-472-087-69	Sequence 69, Appl
37	504	90.6	108	3	US-09-240-274-178	Sequence 178, App
38	501	90.1	108	1	US-07-634-278-86	Sequence 86, Appl
39	501	90.1	108	1	US-08-477-728-86	Sequence 86, Appl
40	501	90.1	108	1	US-08-474-040-86	Sequence 86, Appl
41	501	90.1	108	1	US-08-487-200-86	Sequence 86, Appl
42	501	90.1	108	3	US-08-484-537-86	Sequence 86, Appl
43	499.5	89.8	226	4	US-09-456-090A-80	Sequence 80, Appl
44	499.5	89.8	226	4	US-09-453-234-80	Sequence 80, Appl
45	496.5	89.3	146	4	US-09-472-087-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-456-090A-52
; Sequence 52, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-25L
US-09-456-090A-52

Query Match 94.3%; Score 524.5; DB 4; Length 224;
Best Local Similarity 96.3%; Pred. No. 1.4e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

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Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
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Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIK 107
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RESULT 2
US-09-453-234-52
; Sequence 52, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01

Res 2 - 5

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;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-25L
US-09-453-234-52

  Query Match            94.3%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity  96.3%;  Pred. No. 1.4e-39;
  Matches  104;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              :|||||||||||||||||||||||||||:  ||||||||||||||||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIK 107


RESULT 3
US-09-456-090A-42
; Sequence 42, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-456-090A-42

  Query Match            94.0%;  Score 522.5;  DB 4;  Length 226;
  Best Local Similarity  94.5%;  Pred. No. 2.1e-39;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSS-FTFGPGTKVDIK 108
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Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPIFTFGPGTKVDIK 109


RESULT 4
US-09-453-234-42
; Sequence 42, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-453-234-42

  Query Match            94.0%;  Score 522.5;  DB 4;  Length 226;
  Best Local Similarity  94.5%;  Pred. No. 2.1e-39;
  Matches  103;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSS-FTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | |  ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPIFTFGPGTKVDIK 109


RESULT 5
US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-16
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  Query Match             93.5%;  Score 520;  DB 3;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-39;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||: | | :||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPYTFGQGTKVEIK 108


RESULT 6
US-09-490-070A-16
; Sequence 16, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 109 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-070A-16

  Query Match             93.5%;  Score 520;  DB 4;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-39;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||: | | :||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPYTFGQGTKVEIK 108


RESULT 7
US-09-490-153-16
; Sequence 16, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10021
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,153
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/025,769B
;             FILING DATE: 18-FEB-1998
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: James F. Haley, Jr., Esq.
;             REGISTRATION NUMBER: 27,794
;             REFERENCE/DOCKET NUMBER: MORPHO/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)596-9000
;             TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 109 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-153-16

  Query Match             93.5%;  Score 520;  DB 4;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-39;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
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Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPYTFGQGTKVEIK 108


RESULT 8
US-09-490-324-16
; Sequence 16, Application US/09490324
; Patent No. 6828422
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
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;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,324
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 16:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 109 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-324-16

  Query Match             93.5%;  Score 520;  DB 4;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 1.6e-39;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | | :||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPYTFGQGTKVEIK 108


RESULT 9
US-09-456-090A-76
; Sequence 76, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-16L
US-09-456-090A-76

  Query Match             93.3%;  Score 518.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 4.7e-39;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||| |||||||||||||||||||||||:  ||||||||||||||||
Db         61 DRFSVSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIK 107


RESULT 10
US-09-453-234-76
; Sequence 76, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-16L
US-09-453-234-76

  Query Match             93.3%;  Score 518.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 4.7e-39;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||| |||||||||||||||||||||||:  ||||||||||||||||
Db         61 DRFSVSGSGTDFTLTISRLEPEDFAVYYCQQY-GSSFTFGPGTKVDIK 107


RESULT 11
US-09-456-090A-72
; Sequence 72, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 226
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-11L
US-09-456-090A-72

  Query Match             93.3%;  Score 518.5;  DB 4;  Length 226;
  Best Local Similarity   93.6%;  Pred. No. 4.7e-39;
  Matches  102;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | |  ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109


RESULT 12
US-09-453-234-72
; Sequence 72, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-11L
US-09-453-234-72

  Query Match             93.3%;  Score 518.5;  DB 4;  Length 226;
  Best Local Similarity   93.6%;  Pred. No. 4.7e-39;
  Matches  102;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
              |||:||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||: | |  ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109


RESULT 13
US-09-456-090A-40
; Sequence 40, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-4L
US-09-456-090A-40

  Query Match             93.1%;  Score 517.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 5.7e-39;
  Matches  103;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLHIYGASRRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||:  ||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQF-GSSFTFGPGTKVDIK 107


RESULT 14
US-09-453-234-40
; Sequence 40, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-4L
US-09-453-234-40

  Query Match             93.1%;  Score 517.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 5.7e-39;
  Matches  103;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLHIYGASRRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGSSFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||:  ||||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQF-GSSFTFGPGTKVDIK 107


RESULT 15
US-09-456-090A-38
; Sequence 38, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 38
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3L
US-09-456-090A-38

Query Match 92.9%; Score 516.5; DB 4; Length 226;
Best Local Similarity 93.6%; Pred. No. 7.1e-39;
Matches 102; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

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Db          1 EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQRSGGS-SFTFGPGTKVDIK 108
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Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109
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Search completed: August 18, 2005, 06:22:53
Job time : 61.6784 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 2.80919 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-34
Perfect score: 32
Sequence: 1 SYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	8	3	US-08-444-818-602	Sequence 602, App
2	32	100.0	8	3	US-08-444-818-603	Sequence 603, App
3	32	100.0	8	3	US-08-444-818-604	Sequence 604, App
4	32	100.0	98	1	US-08-478-039-81	Sequence 81, Appl
5	32	100.0	98	1	US-08-476-349A-81	Sequence 81, Appl
6	32	100.0	98	2	US-08-665-202-33	Sequence 33, Appl
7	32	100.0	98	4	US-09-315-574-33	Sequence 33, Appl
8	32	100.0	117	3	US-08-545-809A-133	Sequence 133, App
9	32	100.0	119	3	US-09-025-769B-26	Sequence 26, Appl
10	32	100.0	119	4	US-09-490-070A-26	Sequence 26, Appl
11	32	100.0	119	4	US-09-490-153-26	Sequence 26, Appl
12	32	100.0	119	4	US-09-490-324-26	Sequence 26, Appl
13	32	100.0	120	3	US-09-025-769B-40	Sequence 40, Appl
14	32	100.0	120	3	US-09-025-769B-67	Sequence 67, Appl
15	32	100.0	120	4	US-09-490-070A-40	Sequence 40, Appl
16	32	100.0	120	4	US-09-490-070A-67	Sequence 67, Appl
17	32	100.0	120	4	US-09-490-153-40	Sequence 40, Appl
18	32	100.0	120	4	US-09-490-153-67	Sequence 67, Appl
19	32	100.0	120	4	US-09-490-324-40	Sequence 40, Appl
20	32	100.0	120	4	US-09-490-324-67	Sequence 67, Appl
21	32	100.0	121	1	US-08-388-672A-20	Sequence 20, Appl
22	32	100.0	121	1	US-08-388-672A-23	Sequence 23, Appl
23	32	100.0	121	3	US-09-080-554-23	Sequence 23, Appl
24	32	100.0	122	3	US-08-983-607-30	Sequence 30, Appl
25	32	100.0	126	3	US-09-080-554-20	Sequence 20, Appl
26	32	100.0	165	4	US-09-902-540-9847	Sequence 9847, Ap
27	32	100.0	193	4	US-09-543-681A-4479	Sequence 4479, Ap
28	32	100.0	377	1	US-08-525-697-2	Sequence 2, Appli
29	32	100.0	412	4	US-09-252-991A-22173	Sequence 22173, A
30	32	100.0	427	4	US-09-540-236-1946	Sequence 1946, Ap
31	32	100.0	453	4	US-09-583-110-3842	Sequence 3842, Ap
32	32	100.0	461	4	US-09-107-433-3722	Sequence 3722, Ap
33	31	96.9	192	4	US-09-543-681A-5684	Sequence 5684, Ap
34	31	96.9	204	4	US-09-513-999C-7997	Sequence 7997, Ap
35	31	96.9	204	4	US-09-513-999C-7998	Sequence 7998, Ap
36	31	96.9	456	4	US-09-328-352-6393	Sequence 6393, Ap
37	30	93.8	250	4	US-09-270-767-45176	Sequence 45176, A
38	30	93.8	296	4	US-09-902-540-14636	Sequence 14636, A
39	30	93.8	345	3	US-09-120-365-73	Sequence 73, Appl
40	30	93.8	345	3	US-09-515-039-73	Sequence 73, Appl
41	30	93.8	345	3	US-08-827-171B-7	Sequence 7, Appli
42	30	93.8	345	4	US-09-598-062-7	Sequence 7, Appli
43	30	93.8	743	4	US-09-248-796A-17817	Sequence 17817, A
44	30	93.8	1410	3	US-09-335-409-3	Sequence 3, Appli
45	30	93.8	1410	3	US-09-568-102-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-444-818-602
; Sequence 602, Application US/08444818
; Patent No. 6150087
;  GENERAL INFORMATION:
;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  777
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,818
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,590
;      FILING DATE:  14-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harbin, Alisa A.
;      REGISTRATION NUMBER:  33,895
;      REFERENCE/DOCKET NUMBER:  0110.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)359-3876
;      TELEFAX:  (508)359-3885
;  INFORMATION FOR SEQ ID NO:  602:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-444-818-602

  Query Match           100.0%;  Score 32;  DB 3;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 4.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
```

```
Db          4 SYWIG 8


RESULT 2
US-08-444-818-603
; Sequence 603, Application US/08444818
; Patent No. 6150087
;  GENERAL INFORMATION:
;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  777
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,818
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,590
;      FILING DATE:  14-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harbin, Alisa A.
;      REGISTRATION NUMBER:  33,895
;      REFERENCE/DOCKET NUMBER:  0110.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)359-3876
;      TELEFAX:  (508)359-3885
;  INFORMATION FOR SEQ ID NO:  603:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-444-818-603

  Query Match           100.0%;  Score 32;  DB 3;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 4.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          3 SYWIG 7


RESULT 3
US-08-444-818-604
; Sequence 604, Application US/08444818
; Patent No. 6150087
;  GENERAL INFORMATION:
;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  777
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,818
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,590
;      FILING DATE:  14-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harbin, Alisa A.
;      REGISTRATION NUMBER:  33,895
;      REFERENCE/DOCKET NUMBER:  0110.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)359-3876
;      TELEFAX:  (508)359-3885
;  INFORMATION FOR SEQ ID NO:  604:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-444-818-604

  Query Match           100.0%;  Score 32;  DB 3;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 4.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          2 SYWIG 6


RESULT 4
US-08-478-039-81
; Sequence 81, Application US/08478039
; Patent No. 5681722
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,039
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/379,072
;      FILING DATE:  25-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/912,292
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/856,281
;      FILING DATE:  23-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,064
```

```
;      FILING DATE:  25-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin Esq., Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-160
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  81:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  VH5 consensus
US-08-478-039-81

  Query Match             100.0%;  Score 32;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 5
US-08-476-349A-81
; Sequence 81, Application US/08476349A
; Patent No. 5750105
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,349A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/379,072
;      FILING DATE:  25-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/912,292
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/856,281
;      FILING DATE:  23-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,064
;      FILING DATE:  25-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin Esq., Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-161
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  81:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  VH5 consensus
US-08-476-349A-81

  Query Match             100.0%;  Score 32;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 6
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-33

  Query Match             100.0%;  Score 32;  DB 2;  Length 98;
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```
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 7
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/315,574
;      FILING DATE:  20-MAY-99
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,202
;      FILING DATE:  13-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-315-574-33

  Query Match             100.0%;  Score 32;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 8
US-08-545-809A-133
; Sequence 133, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,809A
;      FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00603
;      FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06501/004001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  133:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-545-809A-133

  Query Match             100.0%;  Score 32;  DB 3;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         50 SYWIG 54


RESULT 9
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-26

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 10
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                       White & McAuliffe
;            STREET: 1666 K Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,070A
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Colin G. Sandercock, Esq.
;            REGISTRATION NUMBER: 31,298
;            REFERENCE/DOCKET NUMBER: 37629-0005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 912-2000
;            TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

  Query Match             100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 11
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,153
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769B
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

  Query Match             100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35
```

```
RESULT 12
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,324
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

  Query Match             100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 13
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-40

  Query Match             100.0%;  Score 32;  DB 3;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 14
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-67

  Query Match            100.0%;  Score 32;  DB 3;  Length 120;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 15
US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

  Query Match            100.0%;  Score 32;  DB 4;  Length 120;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


Search completed: August 18, 2005, 06:22:54
Job time : 3.80919 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 10.7774 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-34
Perfect score: 32
Sequence: 1 SYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	5	4	AAB85351	Aab85351 Antibody
2	32	100.0	5	6	ABU08150	Abu08150 ErbB2 rec
3	32	100.0	5	7	ADD69217	Add69217 Human hea
4	32	100.0	5	7	ADD69223	Add69223 Human hea
5	32	100.0	5	8	ADH89395	Adh89395 Human tra
6	32	100.0	5	8	ADS87941	Ads87941 Anti-IFN-
7	32	100.0	5	8	ADS19294	Ads19294 Heavy cha
8	32	100.0	5	8	ADS94938	Ads94938 Anti-IFN-
9	32	100.0	8	2	AAR36120	Aar36120 Hepatitis
10	32	100.0	8	2	AAR36119	Aar36119 Hepatitis
11	32	100.0	8	2	AAR36118	Aar36118 Hepatitis
12	32	100.0	10	6	ABR01558	Abr01558 Human ant
13	32	100.0	10	8	ADP47172	Adp47172 Human pho
14	32	100.0	10	8	ADP47157	Adp47157 Human pho
15	32	100.0	10	8	ADP47139	Adp47139 Human pho
16	32	100.0	72	4	ABG05924	Abg05924 Novel hum
17	32	100.0	84	2	AAW62797	Aaw62797 Amino aci
18	32	100.0	98	2	AAW54008	Aaw54008 Human Ant
19	32	100.0	98	5	ABG78233	Abg78233 Human Fv
20	32	100.0	98	5	ABG78231	Abg78231 Human Fv
21	32	100.0	98	5	ABG78232	Abg78232 Human Fv
22	32	100.0	98	5	ABG91924	Abg91924 Human ant
23	32	100.0	98	5	ABG91922	Abg91922 Human ant
24	32	100.0	98	5	ABG91923	Abg91923 Human ant
25	32	100.0	98	6	ABU56809	Abu56809 Human Imm
26	32	100.0	98	6	ABP56508	Abp56508 Human ant
27	32	100.0	98	6	ABJ18687	Abj18687 Antibody
28	32	100.0	98	6	ABO27112	Abo27112 Human ger
29	32	100.0	98	7	ADD69247	Add69247 Human hea
30	32	100.0	98	7	ADF10156	Adf10156 Antibody
31	32	100.0	98	7	ADF09948	Adf09948 Antibody
32	32	100.0	98	7	ADF10053	Adf10053 VEGF anti
33	32	100.0	98	7	ADK18943	Adk18943 Anti-huma
34	32	100.0	98	7	ADK18888	Adk18888 Anti-huma
35	32	100.0	98	7	ADK18877	Adk18877 Anti-huma
36	32	100.0	98	7	ADK18878	Adk18878 Anti-huma
37	32	100.0	98	7	ADK18912	Adk18912 Anti-huma
38	32	100.0	98	7	ADK18582	Adk18582 Anti-huma
39	32	100.0	98	7	ADK18890	Adk18890 Anti-huma
40	32	100.0	98	7	ADK18896	Adk18896 Anti-huma
41	32	100.0	98	7	ADK18894	Adk18894 Anti-huma
42	32	100.0	98	7	ADK18914	Adk18914 Anti-huma
43	32	100.0	98	7	ADK18944	Adk18944 Anti-huma
44	32	100.0	98	7	ADJ80328	Adj80328 VH gene 1
45	32	100.0	98	8	ADR46847	Adr46847 Human VH5

ALIGNMENTS

RESULT 1
AAB85351
ID AAB85351 standard; peptide; 5 AA.
XX
AC AAB85351;
XX
DT 17-SEP-2001 (first entry)
XX
DE Antibody AAL 160 heavy chain variable domain CDR1 region.
XX
KW Interleukin 1beta; IL-1beta; antibody AAL 160; immunosuppressive;
KW cerebroprotective; antiinflammatory; antiallergic; antiasthmatic;
KW osteopathic; vasotropic; antiarthritic; dermatological; antithyroid;
KW neuroprotective; vulnerary; immunomodulator; cytostatic; anti-HIV.
XX
OS Homo sapiens.
XX
PN WO200153353-A2.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-EP000591.
XX
PR 21-JAN-2000; 2000GB-00001448.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Gram H, Di Padova FE;
XX
DR WPI; 2001-451903/48.
XX
PT New anti-IL-1beta antibody molecule, comprising at least 1 one
PT immunoglobulin heavy chain variable domain (VH) which comprises
PT hypervariable regions CDR1, CDR2 and CDR3, for treating autoimmune and
PT inflammatory diseases.
XX
PS Claim 1; Page 28; 36pp; English.
XX
CC The invention provides an interleukin 1beta (IL-1beta) binding molecule,
CC in particular a human antibody to human IL-1beta. The IL-1beta binding
CC molecules of the invention are used to treat IL-1 mediated diseases or
CC disorders e.g. septicemia, septic or endotoxic shock, allergies, asthma,
CC bone loss, ischemia, stroke, rheumatoid arthritis, autoimmune diseases
CC (e.g. hemolytic anemia, systemic lupus erythematosus, myasthenia gravis,
CC Crohn's disease, inflammatory bowel syndrome, Graves disease, multiple
CC sclerosis) and inflammatory disorders (e.g. bronchitis and pulmonary
CC emphysema), adult respiratory distress syndrome, meningitis, pneumonia,

```
CC   severe burns, cachexia, cancer, IL-1-dependent tumors and acquired
CC   immunodeficiency syndrome (AIDS)-related cachexia. The IL-1beta binding
CC   molecules may also be used to prevent graft-versus-host disease in
CC   transplant patients. The present sequence represents a complementarity
CC   determining region (CDR) of the heavy chain variable domain of antibody
CC   AAL 160, an IL-1beta binding molecule
XX
SQ   Sequence 5 AA;

  Query Match          100.0%;  Score 32;  DB 4;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5


RESULT 2
ABU08150
ID   ABU08150 standard; peptide; 5 AA.
XX
AC   ABU08150;
XX
DT   10-MAY-2003  (first entry)
XX
DE   ErbB2 receptor antibody VH domain CDR-1.
XX
KW   Human; single-chain antibody; anti-ErbB2 antibody; Erbicin;
KW   growth inhibitor; ErbB2 receptor; transmembrane tyrosine kinase receptor;
KW   RTK; antibody; gene therapy; bacteriophage; antitumour agent; tumour;
KW   mammary carcinoma; ovarian carcinoma; colon carcinoma; lung carcinoma;
KW   salivary gland tumour; gastric tumour; antiproliferative; cytostatic; VH;
KW   CDR; complementarity determining region; variable domain; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2003006509-A2.
XX
PD   23-JAN-2003.
XX
PF   10-JUL-2002; 2002WO-EP007671.
XX
PR   10-JUL-2001; 2001IT-RM000408.
XX
PA   (UYNA-) UNIV NAPOLI STUDI FEDERICO II.
XX
PI   D'alessio G,  Piccoli R,  De Lorenzo C,  Palmer DB,  Ritter MA;
XX
DR   WPI; 2003-221720/21.
DR   N-PSDB; ABX12973.
XX
PT   New recombinant single-chain anti-ErbB2 antibody of human origin, useful
PT   for pharmaceutical and diagnostic use, and as an antitumor agent for
PT   mammary, ovarian, colon, lung carcinomas, salivary gland or gastric
PT   tumors.
XX
PS   Claim 10; Page 8; 47pp; English.
XX
CC   The invention discloses a recombinant single-chain anti-ErbB2 antibody of
CC   human origin able to inhibit growth of cells expressing the ErbB2
CC   receptor, referred to as Erbicin. The ErbB2 transmembrane tyrosine kinase
CC   receptor (RTK) is highly expressed in breast, ovary and lung carcinomas
CC   as well as salivary gland or gastric tumours. The antibodies, new
CC   proteins, nucleotide sequences (gene therapy) and bacteriophage are
CC   useful for pharmaceutical and diagnostic use, and as an antitumour agent,
CC   where the tumour can be mammary, ovarian, colon, lung carcinomas,
CC   salivary gland or gastric tumours. They are also useful in preparing
CC   antiproliferative and antitumour drugs. The sequences presented are the
CC   nucleic acids and encoded polypeptides that were used in the invention to
CC   create the antibody
XX
SQ   Sequence 5 AA;

  Query Match          100.0%;  Score 32;  DB 6;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5


RESULT 3
ADD69217
ID   ADD69217 standard; peptide; 5 AA.
XX
AC   ADD69217;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human heavy chain variable region CDR1 peptide - SEQ ID 21.
XX
KW   monoclonal antibody; heavy chain variable region; light; framework;
KW   complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW   prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW   colon cancer; renal carcinoma; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO2003064606-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-US002448.
XX
PR   28-JAN-2002; 2002US-00059989.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Deo YM,  Graziano R,  Hudson D,  Holmes EH,  Tino WT,  Black A;
XX
DR   WPI; 2003-618360/58.
XX
PT   New isolated human monoclonal antibody comprising a human heavy chain and
PT   a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT   CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT   cancer.
XX
PS   Claim 3; SEQ ID NO 21; 136pp; English.
XX
CC   The invention relates to a novel isolated human monoclonal antibody
CC   comprising a human heavy chain variable region and a human light chain
CC   variable region both comprising FR (framework region)-1, CDR
CC   (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC   sequences. The antibody is directed against the human prostate specific
CC   membrane antigen (PSMA). The monoclonal antibody of the invention
CC   demonstrates cytostatic activity and may be useful for treating or
CC   preventing a disease characterised by the growth of tumour cells such as
CC   cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC   well as duing gene therapy procedures. The current sequence is that of
CC   the human heavy chain variable region CDR1 peptide of the invention.
XX
SQ   Sequence 5 AA;

  Query Match          100.0%;  Score 32;  DB 7;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5


RESULT 4
ADD69223
```

ID ADD69223 standard; peptide; 5 AA.
XX
AC ADD69223;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heavy chain variable region CDR1 peptide - SEQ ID 27.
XX
KW monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 3; SEQ ID NO 27; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as duing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR1 peptide of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 1 SYWIG 5

RESULT 5
ADH89395
ID ADH89395 standard; peptide; 5 AA.
XX
AC ADH89395;
XX
DT 15-APR-2004 (first entry)
XX
DE Human transferrin fusion protein-related CDR1 peptide SeqID39.
XX
KW fusion protein; transferrin protein; glycosylation;
KW antibody variable region; cytostatic; antibacterial; virucide;
KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
KW viral infection; parasitic infection; neoplasm; autoimmune disease;
KW arthritis; graft rejection.
XX
OS Unidentified.
XX
PN US2003226155-A1.
XX
PD 04-DEC-2003.
XX
PF 10-MAR-2003; 2003US-00384060.
XX
PR 30-AUG-2001; 2001US-0315745P.
PR 30-NOV-2001; 2001US-0334059P.
PR 30-AUG-2002; 2002US-00231494.
PR 30-AUG-2002; 2002US-0406977P.
XX
PA (BIOR-) BIOREXIS PHARM CORP.
XX
PI Sadeghi H, Prior CP, Turner A;
XX
DR WPI; 2004-022093/02.
XX
PT New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.
XX
PS Example 2; SEQ ID NO 39; 82pp; English.
XX
CC This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a CDR 1 peptide which was used in the exemplification
CC of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 1 SYWIG 5

RESULT 6
ADS87941
ID ADS87941 standard; peptide; 5 AA.
XX
AC ADS87941;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR1 SEQ ID NO:34.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.

XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 45; SEQ ID NO 34; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 5 AA;

```
  Query Match             100.0%;  Score 32;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5
```

RESULT 7
ADS19294
ID ADS19294 standard; peptide; 5 AA.
XX
AC ADS19294;
XX
DT 18-NOV-2004 (first entry)
XX
DE Heavy chain CDR1 peptide of human mAb 3G6 antibody SeqID 5.
XX
KW human; antibody; mAb 3G6; lymphocyte migration;
KW inflammatory bowel disease; Crohn's disease; gastroenteritis;
KW pulmonary inflammatory disease; asthma; chronic bronchitis;
KW graft rejection; psoriasis; eczema; urticaria; scleroderma;
KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;
KW autoimmune thyroiditis; Behcet's syndrome; viral infection; cancer;
KW neoplastic disease; leukaemia; lymphoma; antiinflammatory; antiasthmatic;
KW immunosuppressive; antipsoriatic; dermatological; neuroprotective;
KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;
KW alphaE integrin; CD103; alphaE-beta7.
XX
OS Homo sapiens.
XX
PN US2003232387-A1.
XX
PD 18-DEC-2003.
XX
PF 14-JUN-2002; 2002US-00173551.
XX
PR 14-JUN-2002; 2002US-00173551.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lu C;
XX
DR WPI; 2004-178738/17.
XX
PT Novel antibody which binds activated alpha-E integrin, specifically to
PT activation-induced epitope on integrin alpha-E chain (CD103), useful for
PT treating inflammatory bowel diseases e.g., Crohn's disease,
PT gastroenteritis.
XX
PS Claim 8; SEQ ID NO 5; 67pp; English.
XX
CC This invention relates to novel antibody and antigen-binding fragments of
CC antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,
CC it refers to the binding of activation induced epitopes present on
CC activated alphaE integrins, where these integrins are activated by
CC exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable
CC growth factors and/ or mitogens. The present invention describes the
CC alphaE-beta7 integrin as a homing receptor that mediates lymphocyte
CC migration to mucosal epithelium. As such, compositions of this invention
CC are useful for treating a subject having an inflammatory bowel disease
CC such as Crohn's disease or gastroenteritis or pulmonary inflammatory
CC diseases such as asthma and chronic bronchitis. Furthermore, such
CC compositions can be used for inhibiting graft rejection, psoriasis,
CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple
CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's
CC syndrome, viral infections, cancer and/or neoplastic diseases such as
CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
CC antiasthmatic, immunosuppressive, antipsoriatic, dermatological,
CC neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and
CC vasotropic activities. This peptide sequence is a human antibody heavy
CC chain complementarity determining region (CDR) that binds the integrin
CC alphaE chain of the invention.
XX
SQ Sequence 5 AA;

```
  Query Match             100.0%;  Score 32;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5
```

RESULT 8
ADS94938
ID ADS94938 standard; peptide; 5 AA.
XX
AC ADS94938;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR1 SEQ ID NO:34.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;

KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 4; SEQ ID NO 34; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 1 SYWIG 5

RESULT 9
AAR36120
ID AAR36120 standard; protein; 8 AA.
XX
AC AAR36120;
XX
DT 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
DE Hepatitis C virus (HCV) epitope.
XX
KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
PN WO9300365-A2.
XX
PD 07-JAN-1993.
XX
PF 24-JUN-1992; 92WO-US005388.
XX
PR 24-JUN-1991; 91US-00722489.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chien DY, Rutter W;
XX
DR WPI; 1993-036334/04.
XX
PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.
XX
PS Example A; Page 38; 80pp; English.
XX
CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In
CC the epitope mapping experiment three different samples of anti-sera were
CC reacted with the peptide octamer, and then incubated with HRP-labelled
CC goat anti-human Ig antisera, to enable detection of binding. This epitope
CC starts from amino acid 2422 of the HCV polyprotein. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 32; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 2 SYWIG 6

RESULT 10
AAR36119
ID AAR36119 standard; protein; 8 AA.
XX
AC AAR36119;
XX
DT 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
DE Hepatitis C virus (HCV) epitope.
XX
KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
PN WO9300365-A2.
XX
PD 07-JAN-1993.
XX
PF 24-JUN-1992; 92WO-US005388.
XX
PR 24-JUN-1991; 91US-00722489.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chien DY, Rutter W;
XX

DR WPI; 1993-036334/04.
XX
PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.
XX
PS Example A; Page 38; 80pp; English.
XX
CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In
CC the epitope mapping experiment three different samples of anti-sera were
CC reacted with the peptide octamer, and then incubated with HRP-labelled
CC goat anti-human Ig antisera, to enable detection of binding. This epitope
CC starts from amino acid 2421 of the HCV polyprotein. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 32; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 3 SYWIG 7

RESULT 11
AAR36118
ID AAR36118 standard; protein; 8 AA.
XX
AC AAR36118;
XX
DT 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
DE Hepatitis C virus (HCV) epitope.
XX
KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
PN WO9300365-A2.
XX
PD 07-JAN-1993.
XX
PF 24-JUN-1992; 92WO-US005388.
XX
PR 24-JUN-1991; 91US-00722489.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chien DY, Rutter W;
XX
DR WPI; 1993-036334/04.
XX
PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.
XX
PS Example A; Page 38; 80pp; English.
XX
CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In
CC the epitope mapping experiment three different samples of anti-sera were
CC reacted with the peptide octamer, and then incubated with HRP-labelled
CC goat anti-human Ig antisera, to enable detection of binding. This epitope
CC starts from amino acid 2420 of the HCV polyprotein. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 32; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 4 SYWIG 8

RESULT 12
ABR01558
ID ABR01558 standard; peptide; 10 AA.
XX
AC ABR01558;
XX
DT 16-APR-2003 (first entry)
XX
DE Human anti-TIMP-1 Fab VLCDR3 #46.
XX
KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
KW variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;
KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
XX
OS Homo sapiens.
XX
PN WO200286085-A2.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-US012801.
XX
PR 24-APR-2001; 2001US-0285683P.
XX
PA (FARB) BAYER CORP.
PA (MORP-) MORPHOSYS AG.
XX
PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
XX
DR WPI; 2003-129114/12.
XX
PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.
XX
PS Claim 17; Page 226; 228pp; English.
XX
CC The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)
CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP
CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
CC variable light chain (VLC)DR3 region. An antibody preparation of the
CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
CC activity. The human antibody is useful for decreasing an MMP-inhibiting
CC activity of a TIMP-1. It is especially useful for ameliorating the
CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
CC sequences shown in ABR01407-ABR01449 and ABR01555-ABR01569 represent
CC VLCDR regions of an antibody of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 32; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 6 SYWIG 10

```
RESULT 13
ADP47172
ID   ADP47172 standard; peptide; 10 AA.
XX
AC   ADP47172;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific mAb heavy chain peptide #37.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Landes GM,  Haak-Frendscho M,  Chen L,  Lee YR,  Liang ML,  Feng X;
PI   Jia X,  Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Example 5; SEQ ID NO 87; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   amino acid sequence represents a human PLA2-specific monoclonal antibody
CC   heavy chain peptide.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 14
ADP47157
ID   ADP47157 standard; peptide; 10 AA.
XX
AC   ADP47157;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific mAb heavy chain peptide #22.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Landes GM,  Haak-Frendscho M,  Chen L,  Lee YR,  Liang ML,  Feng X;
PI   Jia X,  Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Example 5; SEQ ID NO 72; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   amino acid sequence represents a human PLA2-specific monoclonal antibody
CC   heavy chain peptide.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 15
ADP47139
ID   ADP47139 standard; peptide; 10 AA.
XX
AC   ADP47139;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific mAb heavy chain peptide #4.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
```

PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 54; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC heavy chain peptide.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 32; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10
```

Search completed: August 18, 2005, 06:09:13
Job time : 12.7774 secs

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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 9.38163 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-34
Perfect score: 32
Sequence: 1 SYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	70	2	Q70IK4	Q70ik4 proteus mir
2	32	100.0	70	2	Q70IK5	Q70ik5 shewanella
3	32	100.0	129	1	YPUC_BACSU	P35152 bacillus su
4	32	100.0	129	2	Q8XLG4	Q8xlg4 clostridium
5	32	100.0	152	2	Q9AMR6	Q9amr6 bradyrhizob
6	32	100.0	175	2	Q6P3B5	Q6p3b5 mus musculu
7	32	100.0	205	2	Q8XX14	Q8xx14 ralstonia s
8	32	100.0	211	2	Q8KQY1	Q8kqy1 vibrio chol
9	32	100.0	212	2	Q7NEB2	Q7neb2 gloeobacter
10	32	100.0	214	2	Q8RL12	Q8rl12 providencia
11	32	100.0	246	2	Q75XS2	Q75xs2 equus cabal
12	32	100.0	265	2	Q62978	Q62978 rattus norv
13	32	100.0	266	1	KLR5_MOUSE	Q60652 mus musculu
14	32	100.0	266	1	KLR6_MOUSE	Q60653 mus musculu
15	32	100.0	266	1	KLR8_MOUSE	Q60682 mus musculu
16	32	100.0	266	2	Q6IVG1	Q6ivg1 mus musculu
17	32	100.0	266	2	Q9JHV3	Q9jhv3 mus musculu
18	32	100.0	266	2	Q9R1G6	Q9r1g6 mus musculu
19	32	100.0	273	2	Q6DUV0	Q6duv0 mus musculu
20	32	100.0	273	2	Q6IVG2	Q6ivg2 mus musculu
21	32	100.0	273	2	Q9JMA4	Q9jma4 mus musculu
22	32	100.0	274	2	Q8BJS9	Q8bjs9 mus musculu
23	32	100.0	280	2	Q75XR4	Q75xr4 equus cabal
24	32	100.0	280	2	Q75XR5	Q75xr5 equus cabal
25	32	100.0	280	2	Q75XR8	Q75xr8 equus cabal
26	32	100.0	280	2	Q75XR9	Q75xr9 equus cabal
27	32	100.0	280	2	Q8K3G1	Q8k3g1 rattus norv
28	32	100.0	282	2	Q75XS0	Q75xs0 equus cabal
29	32	100.0	282	2	Q75XS1	Q75xs1 equus cabal
30	32	100.0	282	2	Q75XS3	Q75xs3 equus cabal
31	32	100.0	293	2	Q75XR1	Q75xr1 equus cabal
32	32	100.0	294	2	Q75XR2	Q75xr2 equus cabal
33	32	100.0	295	2	Q8DIG0	Q8dig0 synechococc
34	32	100.0	303	2	Q40953	Q40953 porphyra pu
35	32	100.0	311	2	P72611	P72611 synechocyst
36	32	100.0	313	2	Q9LCD2	Q9lcd2 ochrobactru
37	32	100.0	314	2	Q6MP27	Q6mp27 bdellovibri
38	32	100.0	331	2	Q9ZJ09	Q9zj09 rhodococcus
39	32	100.0	331	2	Q8YTT6	Q8ytt6 anabaena sp
40	32	100.0	377	2	Q00012	Q00012 aspergillus
41	32	100.0	427	2	Q7QLW9	Q7qlw9 anopheles g
42	32	100.0	427	2	Q8VS09	Q8vs09 klebsiella
43	32	100.0	429	1	EXG_KLULA	Q12628 kluyveromyc
44	32	100.0	437	2	Q9HX16	Q9hx16 pseudomonas
45	32	100.0	453	2	Q97QN5	Q97qn5 streptococc

ALIGNMENTS

RESULT 1
Q70IK4
ID Q70IK4 PRELIMINARY; PRT; 70 AA.
AC Q70IK4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative conjugative transfer protein (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711525; DOI=10.1016/j.plasmid.2003.10.003;
RA Boltner D., Osborn A.M.;
RT "Structural comparison of the integrative and conjugative elements
RT R391, pMERPH, R997, and SXT.";
RL Plasmid 51:12-23(2004).
DR EMBL; AJ579930; CAE30343.1; -.
FT NON_TER 70 70
SQ SEQUENCE 70 AA; 8005 MW; 762A88CD4E451C4A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SYWIG 5
              |||||
Db         50 SYWIG 54
```

RESULT 2
Q70IK5
ID Q70IK5 PRELIMINARY; PRT; 70 AA.
AC Q70IK5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative conjugative transfer protein (Fragment).
OS Shewanella putrefaciens (Pseudomonas putrefaciens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=24;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711525; DOI=10.1016/j.plasmid.2003.10.003;
RA Boltner D., Osborn A.M.;
RT "Structural comparison of the integrative and conjugative elements
RT R391, pMERPH, R997, and SXT.";
RL Plasmid 51:12-23(2004).
DR EMBL; AJ579929; CAE30342.1; -.
FT NON_TER 70 70
SQ SEQUENCE 70 AA; 8105 MW; 762A88DD4F451C4A CRC64;

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  Query Match             100.0%;  Score 32;  DB 2;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         50 SYWIG 54


RESULT 3
YPUC_BACSU
ID   YPUC_BACSU     STANDARD;      PRT;   129 AA.
AC   P35152;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hypothetical protein ypuC (ORFX2).
GN   Name=ypuC; OrderedLocusNames=BSU23330;
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168 / Marburg;
RX   MEDLINE=95020538; PubMed=7934829;
RA   Sorokin A.V., Zumstein E., Azevedo V., Ehrlich S.D., Serror P.;
RT   "The organization of the Bacillus subtilis 168 chromosome region
RT   between the spoVA and serA genetic loci, based on sequence data.";
RL   Mol. Microbiol. 10:385-395(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA   Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA   Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA   Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA   Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA   Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA   Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA   Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA   Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA   Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA   Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA   Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA   Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA   Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA   Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA   Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA   Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA   Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA   Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L09228; AAA67477.1; -.
DR   EMBL; Z99116; CAB14265.1; -.
DR   PIR; S45539; S45539.
DR   SubtiList; BG10514; ypuC.
DR   InterPro; IPR008934; AcPase_VanPerase.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   129 AA;  14831 MW;  FAEBD3A9E9E810AB CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          2 SYWIG 6


RESULT 4
Q8XLG4
ID   Q8XLG4      PRELIMINARY;      PRT;   129 AA.
AC   Q8XLG4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein CPE1077.
GN   OrderedLocusNames=CPE1077;
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13 / Type A;
RX   MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR   EMBL; AP003189; BAB80783.1; -.
DR   Pfam; PF03551; PadR; 1.
KW   Complete proteome.
SQ   SEQUENCE   129 AA;  15154 MW;  1D293EC6E78458ED CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         76 SYWIG 80


RESULT 5
Q9AMR6
ID   Q9AMR6      PRELIMINARY;      PRT;   152 AA.
AC   Q9AMR6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ID927.
GN   Name=id927;
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=110spc4;
RX   MEDLINE=21101824; PubMed=11157954;
RX   DOI=10.1128/JB.183.4.1405-1412.2001;
```

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RA   Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA   Hennecke H.;
RT   "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT   DNA region of the Bradyrhizobium japonicum chromosome.";
RL   J. Bacteriol. 183:1405-1412(2001).
DR   EMBL; AF322013; AAG61081.1; -.
SQ   SEQUENCE   152 AA;  16298 MW;  11B34FA514394C88 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          9 SYWIG 13


RESULT 6
Q6P3B5
ID   Q6P3B5      PRELIMINARY;      PRT;   175 AA.
AC   Q6P3B5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC064073; AAH64073.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   175 AA;  20810 MW;  B82BA0246E7A63CF CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 175;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        108 SYWIG 112


RESULT 7
Q8XX14
ID   Q8XX14      PRELIMINARY;      PRT;   205 AA.
AC   Q8XX14;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   PUTATIVE PROLINE RICH TRANSMEMBRANE PROTEIN.
GN   Name=RS01248; OrderedLocusNames=RSc2304;
OS   Ralstonia solanacearum (Pseudomonas solanacearum).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Ralstonia.
OX   NCBI_TaxID=305;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GMI1000;
RX   MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA   Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA   Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA   Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA   Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA   Weissenbach J., Boucher C.A.;
RT   "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL   Nature 415:497-502(2002).
DR   EMBL; AL646069; CAD16011.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
KW   Complete proteome; Transmembrane.
SQ   SEQUENCE   205 AA;  21129 MW;  58510CBE0FCD0B9B CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 205;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         16 SYWIG 20


RESULT 8
Q8KQY1
ID   Q8KQY1      PRELIMINARY;      PRT;   211 AA.
AC   Q8KQY1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Putative conjugation coupling factor.
GN   Name=s043;
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22103115; PubMed=12107144;
RX   DOI=10.1128/JB.184.15.4259-4269.2002;
RA   Beaber J.W., Hochhut B., Waldor M.K.;
RT   "Genomic and functional analyses of SXT, an integrating antibiotic
RT   resistance gene transfer element derived from Vibrio cholerae.";
RL   J. Bacteriol. 184:4259-4269(2002).
DR   EMBL; AY055428; AAL59721.1; -.
SQ   SEQUENCE   211 AA;  24119 MW;  A4A6A14464055F2F CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 211;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         50 SYWIG 54
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RESULT 9
Q7NEB2
ID   Q7NEB2      PRELIMINARY;      PRT;   212 AA.
AC   Q7NEB2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ATP-dependent protease.
GN   OrderedLocusNames=glr3968;
OS   Gloeobacter violaceus.
OC   Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX   NCBI_TaxID=33072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 7421;
RX   MEDLINE=22977040; PubMed=14621292;
RA   Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA   Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA   Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT   cyanobacterium that lacks thylakoids.";
RL   DNA Res. 10:137-145(2003).
DR   EMBL; AP006581; BAC91909.1; -.
DR   GO; GO:0004176; F:ATP-dependent peptidase activity; IEA.
DR   GO; GO:0006510; P:ATP-dependent proteolysis; IEA.
DR   InterPro; IPR003111; Pept_S16_N.
DR   Pfam; PF02190; LON; 1.
KW   Complete proteome; Protease.
SQ   SEQUENCE   212 AA;  24277 MW;  7D7F556B45E6A81E CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 212;
  Best Local Similarity  100.0%;  Pred. No. 5.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        160 SYWIG 164


RESULT 10
Q8RL12
ID   Q8RL12      PRELIMINARY;      PRT;   214 AA.
AC   Q8RL12;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Providencia rettgeri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Providencia.
OX   NCBI_TaxID=587;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22181475; PubMed=12193633;
RX   DOI=10.1128/JB.184.18.5158-5169.2002;
RA   Boltner D., MacMahon C., Pembroke J.T., Strike P., Osborn A.M.;
RT   "R391: a Conjugative Integrating Mosaic Comprised of Phage, Plasmid,
RT   and Transposon Elements.";
RL   J. Bacteriol. 184:5158-5169(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Boeltner D., MacMahon C., Pembroke J.T., Strike P., Osborn A.M.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY090559; AAM08039.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   214 AA;  24615 MW;  351744D91E039377 CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 214;
  Best Local Similarity  100.0%;  Pred. No. 5.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         53 SYWIG 57


RESULT 11
Q75XS2
ID   Q75XS2      PRELIMINARY;      PRT;   246 AA.
AC   Q75XS2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Killer cell lectin-like receptor.
GN   Name=Ly49B;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   PubMed=14991607; DOI=10.1002/eji.200324695;
RA   Takahashi T., Yawata M., Raudsepp T., Lear T.L., Chowdhary B.P.,
RA   Antczak D.F., Kasahara M.;
RT   "Natural killer cell receptors in the horse: evidence for the
RT   existence of multiple transcribed LY49 genes.";
RL   Eur. J. Immunol. 34:773-784(2004).
DR   EMBL; AB120382; BAD12812.1; -.
DR   HSSP; Q13241; 1B6E.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Lectin; Receptor.
SQ   SEQUENCE   246 AA;  28780 MW;  5E098D3870E6F8E5 CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 246;
  Best Local Similarity  100.0%;  Pred. No. 6.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        208 SYWIG 212


RESULT 12
Q62978
ID   Q62978      PRELIMINARY;      PRT;   265 AA.
AC   Q62978;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ly-49.12 antigen.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F344;
RX   MEDLINE=96235029; PubMed=8642329;
RA   Dissen E., Ryan J.C., Seaman W.E., Fossum S.;
RT   "An autosomal dominant locus, Nka, mapping to the Ly-49 region of a
RT   rat natural killer (NK) gene complex, controls NK cell lysis of
RT   allogeneic lymphocytes.";
RL   J. Exp. Med. 183:2197-2207(1996).
DR   EMBL; U56822; AAB07361.1; -.
DR   HSSP; Q9JHN9; 1JA3.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
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DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   265 AA;  31250 MW;  C768E9AA86BF2C4B CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        197 SYWIG 201


RESULT 13
KLR5_MOUSE
ID   KLR5_MOUSE     STANDARD;      PRT;   266 AA.
AC   Q60652;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Killer cell lectin-like receptor 5 (T-cell surface glycoprotein Ly-
DE   49E) (Ly49-E antigen) (Lymphocyte antigen 49E).
GN   Name=Klra5; Synonyms=Ly-49e, Ly49-e, Ly49e;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=94300068; PubMed=8027540;
RA   Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
RT   "Ly-49 multigene family expressed by IL-2-activated NK cells.";
RL   J. Immunol. 153:1068-1079(1994).
CC   -!- FUNCTION: Receptor on natural killer (NK) cells for class I MHC.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U10091; AAA50219.1; -.
DR   PIR; I49050; I49050.
DR   HSSP; Q9JHN9; 1JA3.
DR   MGD; MGI:101903; Klra5.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Antigen; Cell adhesion; Glycoprotein; Lectin; Multigene family;
KW   Receptor; Signal-anchor; T-cell; Transmembrane.
FT   DOMAIN        1     44       Cytoplasmic (Potential).
FT   TRANSMEM     45     66       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   DOMAIN       67    266       Extracellular (Potential).
FT   DOMAIN      143    261       C-type lectin.
FT   DISULFID    171    257       By similarity.
FT   DISULFID    236    249       By similarity.
FT   CARBOHYD     87     87       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    250    250       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   266 AA;  30843 MW;  B8B07F221875049C CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 266;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        198 SYWIG 202


RESULT 14
KLR6_MOUSE
ID   KLR6_MOUSE     STANDARD;      PRT;   266 AA.
AC   Q60653;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Killer cell lectin-like receptor 6 (T-cell surface glycoprotein Ly-
DE   49F) (Ly49-F antigen) (Lymphocyte antigen 49F).
GN   Name=Klra6; Synonyms=Ly-49f, Ly49-f, Ly49F;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=94300068; PubMed=8027540;
RA   Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
RT   "Ly-49 multigene family expressed by IL-2-activated NK cells.";
RL   J. Immunol. 153:1068-1079(1994).
CC   -!- FUNCTION: Receptor on natural killer (NK) cells for class I MHC.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U10092; AAA50220.1; -.
DR   PIR; I49051; I49051.
DR   HSSP; Q9JHN9; 1JA3.
DR   MGD; MGI:101902; Klra6.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Antigen; Cell adhesion; Glycoprotein; Lectin; Multigene family;
KW   Receptor; Signal-anchor; T-cell; Transmembrane.
FT   DOMAIN        1     44       Cytoplasmic (Potential).
FT   TRANSMEM     45     66       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   DOMAIN       67    266       Extracellular (Potential).
FT   DOMAIN      143    261       C-type lectin.
FT   DISULFID    171    257       By similarity.
FT   DISULFID    236    249       By similarity.
FT   CARBOHYD     87     87       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   266 AA;  31269 MW;  AD180AA9C762F1F6 CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 266;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        198 SYWIG 202


RESULT 15
KLR8_MOUSE
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ID   KLR8_MOUSE     STANDARD;      PRT;   266 AA.
AC   Q60682; O78027;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Killer cell lectin-like receptor 8 (T-cell surface glycoprotein Ly-
DE   49H) (Ly49-H antigen) (Lymphocyte antigen 49H).
GN   Name=Klra8; Synonyms=Ly-49h, Ly49-h, Ly49H;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM H1).
RC   STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX   MEDLINE=95053763; PubMed=7964501;
RA   Brennan J., Mager D., Jefferies W., Takei F.;
RT   "Expression of different members of the Ly-49 gene family defines
RT   distinct natural killer cell subsets and cell adhesion properties.";
RL   J. Exp. Med. 180:2287-2295(1994).
RN   [2]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   STRAIN=C57BL/6;
RX   MEDLINE=96421544; PubMed=8824161; DOI=10.1007/s002510050156;
RA   Silver E.T., Elliott J.F., Kane K.P.;
RT   "Alternatively spliced Ly-49D and H transcripts are found in IL-2-
RT   activated NK cells.";
RL   Immunogenetics 44:478-482(1996).
CC   -!- FUNCTION: Receptor on natural killer (NK) cells for class I MHC.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=H1;
CC         IsoId=Q60682-1; Sequence=Displayed;
CC       Name=H2;
CC         IsoId=Q60682-2; Sequence=VSP_003071;
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U12889; AAA58704.1; -.
DR   EMBL; L78253; AAC32668.1; -.
DR   PIR; I49114; I49114.
DR   HSSP; Q9JHN9; 1JA3.
DR   MGD; MGI:102968; Klra8.
DR   GO; GO:0009615; P:response to virus; IDA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Alternative splicing; Antigen; Cell adhesion; Glycoprotein; Lectin;
KW   Multigene family; Receptor; Signal-anchor; T-cell; Transmembrane.
FT   DOMAIN        1     44       Cytoplasmic (Potential).
FT   TRANSMEM     45     66       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   DOMAIN       67    266       Extracellular (Potential).
FT   DOMAIN      143    261       C-type lectin.
FT   DISULFID    171    257       By similarity.
FT   DISULFID    236    249       By similarity.
FT   CARBOHYD     87     87       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     39     41       Missing (in isoform H2).
FT                                /FTId=VSP_003071.
SQ   SEQUENCE   266 AA;  31393 MW;  3CB5A8EF2EB401E2 CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 266;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db        198 SYWIG 202


Search completed: August 18, 2005, 06:18:11
Job time : 11.3816 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 9.46996 Seconds
(without alignments)
206.752 Million cell updates/sec

Title: US-10-684-957-34
Perfect score: 32
Sequence: 1 SYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	5	15	US-10-384-060-39	Sequence 39, Appl
2	32	100.0	5	15	US-10-173-551-5	Sequence 5, Appli
3	32	100.0	5	17	US-10-684-957-34	Sequence 34, Appl
4	32	100.0	10	16	US-10-128-520-367	Sequence 367, App
5	32	100.0	10	17	US-10-638-265-89	Sequence 89, Appl
6	32	100.0	10	17	US-10-726-332-54	Sequence 54, Appl
7	32	100.0	10	17	US-10-726-332-72	Sequence 72, Appl
8	32	100.0	10	17	US-10-726-332-87	Sequence 87, Appl
9	32	100.0	82	14	US-10-078-958-5	Sequence 5, Appli
10	32	100.0	97	15	US-10-424-599-195081	Sequence 195081,
11	32	100.0	98	9	US-09-850-165-89	Sequence 89, Appl
12	32	100.0	98	14	US-10-194-975-45	Sequence 45, Appl
13	32	100.0	98	14	US-10-125-687-16	Sequence 16, Appl
14	32	100.0	98	14	US-10-041-860-6	Sequence 6, Appli
15	32	100.0	98	14	US-10-041-860-301	Sequence 301, App
16	32	100.0	98	14	US-10-041-860-302	Sequence 302, App
17	32	100.0	98	14	US-10-041-860-312	Sequence 312, App
18	32	100.0	98	14	US-10-041-860-314	Sequence 314, App
19	32	100.0	98	14	US-10-041-860-318	Sequence 318, App
20	32	100.0	98	14	US-10-041-860-320	Sequence 320, App
21	32	100.0	98	14	US-10-041-860-336	Sequence 336, App
22	32	100.0	98	14	US-10-041-860-338	Sequence 338, App
23	32	100.0	98	14	US-10-041-860-367	Sequence 367, App
24	32	100.0	98	14	US-10-041-860-368	Sequence 368, App
25	32	100.0	98	15	US-10-308-817-88	Sequence 88, Appl
26	32	100.0	98	15	US-10-032-037B-106	Sequence 106, App
27	32	100.0	98	15	US-10-032-037B-107	Sequence 107, App
28	32	100.0	98	15	US-10-032-037B-108	Sequence 108, App
29	32	100.0	98	15	US-10-029-988B-106	Sequence 106, App
30	32	100.0	98	15	US-10-029-988B-107	Sequence 107, App
31	32	100.0	98	15	US-10-029-988B-108	Sequence 108, App
32	32	100.0	98	15	US-10-032-423A-106	Sequence 106, App
33	32	100.0	98	15	US-10-032-423A-107	Sequence 107, App
34	32	100.0	98	15	US-10-032-423A-108	Sequence 108, App
35	32	100.0	98	15	US-10-453-698-88	Sequence 88, Appl
36	32	100.0	98	15	US-10-029-926B-106	Sequence 106, App
37	32	100.0	98	15	US-10-029-926B-107	Sequence 107, App
38	32	100.0	98	15	US-10-029-926B-108	Sequence 108, App
39	32	100.0	98	16	US-10-379-392-53	Sequence 53, Appl
40	32	100.0	98	16	US-10-769-144-30	Sequence 30, Appl
41	32	100.0	98	18	US-10-996-191-16	Sequence 16, Appl
42	32	100.0	109	16	US-10-800-197-144	Sequence 144, App
43	32	100.0	109	16	US-10-800-197-145	Sequence 145, App
44	32	100.0	109	16	US-10-800-197-146	Sequence 146, App
45	32	100.0	109	17	US-10-727-155-283	Sequence 283, App

ALIGNMENTS

RESULT 1
US-10-384-060-39
; Sequence 39, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 sequence
US-10-384-060-39

Query Match 100.0%; Score 32; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5


RESULT 2
US-10-173-551-5
; Sequence 5, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Chafen
;  TITLE OF INVENTION: Antibodies that bind alphaE Integrin
;  FILE REFERENCE: 1855.2025-000
;  CURRENT APPLICATION NUMBER: US/10/173,551
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-173-551-5

  Query Match             100.0%;  Score 32;  DB 15;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
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Db          1 SYWIG 5


RESULT 3
US-10-684-957-34
; Sequence 34, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-34

  Query Match             100.0%;  Score 32;  DB 17;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          1 SYWIG 5


RESULT 4
US-10-128-520-367
; Sequence 367, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
;  APPLICANT: PAN et al.
;  TITLE OF INVENTION: Human TIMP-1 Antibodies
;  FILE REFERENCE: 02973.00073
;  CURRENT APPLICATION NUMBER: US/10/128,520
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: US 60/285,683
;  PRIOR FILING DATE: 2001-04-24
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-520-367

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  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 5
US-10-638-265-89
; Sequence 89, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
;  APPLICANT: Roskos, Lorin
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  King, Chadwick
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
;  TITLE OF INVENTION:  HORMONE (PTH) AND USES THEREOF
;  FILE REFERENCE: ABGENIX.092A
;  CURRENT APPLICATION NUMBER: US/10/638,265
;  CURRENT FILING DATE:  2003-08-08
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homosapien
US-10-638-265-89

  Query Match             100.0%;  Score 32;  DB 17;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 6
US-10-726-332-54
; Sequence 54, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
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;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-54

  Query Match             100.0%;  Score 32;  DB 17;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 7
US-10-726-332-72
; Sequence 72, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-72

  Query Match             100.0%;  Score 32;  DB 17;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 8
US-10-726-332-87
; Sequence 87, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-87

  Query Match             100.0%;  Score 32;  DB 17;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db          6 SYWIG 10


RESULT 9
US-10-078-958-5
; Sequence 5, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-078-958-5

  Query Match             100.0%;  Score 32;  DB 14;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         15 SYWIG 19


RESULT 10
US-10-424-599-195081
; Sequence 195081, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195081
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Glycine max
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```
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_18185C.1.pep
US-10-424-599-195081

  Query Match             100.0%;  Score 32;  DB 15;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         82 SYWIG 86


RESULT 11
US-09-850-165-89
; Sequence 89, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
;  APPLICANT: NEWMAN, ROLAND A.
;  APPLICANT:  HANNA, NABIL
;  APPLICANT:  RAAB, RONALD W.
;  TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
;  FILE REFERENCE: 037003-0280614
;  CURRENT APPLICATION NUMBER: US/09/850,165
;  CURRENT FILING DATE:  2001-05-08
;  PRIOR APPLICATION NUMBER: 09/082,472
;  PRIOR FILING DATE: 1998-05-21
;  PRIOR APPLICATION NUMBER: 08/476,237
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/397,072
;  PRIOR FILING DATE: 1995-04-17
;  PRIOR APPLICATION NUMBER: 07/912,292
;  PRIOR FILING DATE: 1992-07-10
;  PRIOR APPLICATION NUMBER: 07/856,281
;  PRIOR FILING DATE: 1992-03-23
;  PRIOR APPLICATION NUMBER: 07/735,064
;  PRIOR FILING DATE: 1991-07-25
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (19)
;   OTHER INFORMATION: Arg or Lys
US-09-850-165-89

  Query Match             100.0%;  Score 32;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 12
US-10-194-975-45
; Sequence 45, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-45

  Query Match             100.0%;  Score 32;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 13
US-10-125-687-16
; Sequence 16, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Peter
;  TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
;  FILE REFERENCE: 26050-705
;  CURRENT APPLICATION NUMBER: US/10/125,687
;  CURRENT FILING DATE:  2002-04-17
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-125-687-16

  Query Match             100.0%;  Score 32;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 14
US-10-041-860-6
; Sequence 6, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-6

  Query Match             100.0%;  Score 32;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
```

```
Db         31 SYWIG 35


RESULT 15
US-10-041-860-301
; Sequence 301, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-301

  Query Match            100.0%;  Score 32;  DB 14;  Length 98;
  Best Local Similarity  100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


Search completed: August 18, 2005, 07:08:03
Job time : 9.59496 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 1.99647 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-34
Perfect score: 32
Sequence: 1 SYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	86	2	S12580	Ig heavy chain V r
2	32	100.0	98	2	PH1274	Ig heavy chain V r
3	32	100.0	98	2	S26907	Ig heavy chain V r
4	32	100.0	101	2	S12428	Ig heavy chain V r
5	32	100.0	101	2	S12424	Ig heavy chain V r
6	32	100.0	102	2	PH1266	Ig heavy chain V r
7	32	100.0	102	2	PH1279	Ig heavy chain V r
8	32	100.0	102	2	PH1281	Ig heavy chain V r
9	32	100.0	102	2	PH1244	Ig heavy chain V r
10	32	100.0	102	2	PH1247	Ig heavy chain V r
11	32	100.0	102	2	PH1282	Ig heavy chain V r
12	32	100.0	102	2	PH1275	Ig heavy chain V r
13	32	100.0	102	2	PH1264	Ig heavy chain V r
14	32	100.0	102	2	PH1259	Ig heavy chain V r
15	32	100.0	102	2	PH1241	Ig heavy chain V r
16	32	100.0	102	2	PH1243	Ig heavy chain V r
17	32	100.0	102	2	PH1273	Ig heavy chain V r
18	32	100.0	102	2	PH1265	Ig heavy chain V r
19	32	100.0	102	2	PH1249	Ig heavy chain V r
20	32	100.0	102	2	PH1254	Ig heavy chain V r
21	32	100.0	102	2	PH1252	Ig heavy chain V r
22	32	100.0	102	2	PH1271	Ig heavy chain V r
23	32	100.0	102	2	PH1278	Ig heavy chain V r
24	32	100.0	104	2	B36006	Ig heavy chain V r
25	32	100.0	109	2	PH1672	Ig heavy chain V r
26	32	100.0	113	2	PH1428	Ig heavy chain V r
27	32	100.0	115	2	PH1557	Ig heavy chain V r
28	32	100.0	123	2	S38492	Ig heavy chain - h
29	32	100.0	123	2	C36006	Ig heavy chain V r
30	32	100.0	128	2	S16685	Ig heavy chain V r
31	32	100.0	129	2	S45539	hypothetical prote
32	32	100.0	136	2	A49047	Ig heavy chain V r
33	32	100.0	136	2	PH1559	Ig heavy chain V r
34	32	100.0	139	2	PH1558	Ig heavy chain V r
35	32	100.0	266	2	I49363	natural killer cel
36	32	100.0	266	2	I49114	Ly49H - mouse
37	32	100.0	266	2	I49050	Ly-49E-GE antigen
38	32	100.0	266	2	I49051	Ly-49F-GE antigen
39	32	100.0	311	2	S74459	iron(III) dicitrat
40	32	100.0	331	2	AD2134	iron(III) dicitrat
41	32	100.0	437	2	H83143	hypothetical prote
42	32	100.0	453	2	B95135	MATE efflux family
43	32	100.0	453	2	D98003	conserved hypothet
44	32	100.0	1872	2	T30888	vitellogenin - Ath
45	32	100.0	2223	2	A47447	calcium channel pr

ALIGNMENTS

RESULT 1
S12580
Ig heavy chain V region (26-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-May-1997
C;Accession: S12580
R;Deane, M.; Norton, J.D.
Nucleic Acids Res. 18, 1652, 1990
A;Title: Immunoglobulin heavy chain gene rearrangement involving V-V region recombinatio
A;Reference number: S12580; MUID:90221916; PMID:2109314
A;Accession: S12580
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-86 <DEA>
A;Cross-references: EMBL:X51454
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 5 SYWIG 9

RESULT 2
PH1274
Ig heavy chain V region (clone PBL5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1274
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1274
A;Molecule type: DNA
A;Residues: 1-98 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 35 SYWIG 39

```
RESULT 3
S26907
Ig heavy chain V region (DP-73) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26907
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26907
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12373; NID:g32965; PIDN:CAA78243.1; PID:g32966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         31 SYWIG 35


RESULT 4
S12428
Ig heavy chain V region (5JB) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S12428
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12428
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56367
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         34 SYWIG 38


RESULT 5
S12424
Ig heavy chain V region (5) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C;Accession: S12424; S12425; S12426; S12427; S12429; S12432
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12424
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56372
A;Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
A;Accession: S12425
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA2>
A;Cross-references: EMBL:X56373
A;Accession: S12426
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA3>
A;Cross-references: EMBL:X56370
A;Accession: S12427
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA4>
A;Cross-references: EMBL:X56368
A;Accession: S12429
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA5>
A;Cross-references: EMBL:X56369
A;Accession: S12432
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA6>
A;Cross-references: EMBL:X56371
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         34 SYWIG 38


RESULT 6
PH1266
Ig heavy chain V region (clone VERG5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1266
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1266
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         35 SYWIG 39


RESULT 7
PH1279
Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-1
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1279
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
```

A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1279
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 35 SYWIG 39

RESULT 8
PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1281
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1281
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 35 SYWIG 39

RESULT 9
PH1244
Ig heavy chain V region (clone CORD2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1244
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1244
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 35 SYWIG 39

RESULT 10
PH1247
Ig heavy chain V region (clone CORD5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1247
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1247
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 35 SYWIG 39

RESULT 11
PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWIG 5
|||||
Db 35 SYWIG 39

RESULT 12
PH1275
Ig heavy chain V region (clone PBL6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1275
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1275
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 102;

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  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         35 SYWIG 39


RESULT 13
PH1264
Ig heavy chain V region (clone VERG3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1264
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1264
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         35 SYWIG 39


RESULT 14
PH1259
Ig heavy chain V region (clone CD-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1259
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1259
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         35 SYWIG 39


RESULT 15
PH1241
Ig heavy chain V region (clone CLL10) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1241
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1241
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: B cell chronic lymphocytic leukemia
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 32;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYWIG 5
              |||||
Db         35 SYWIG 39


Search completed: August 18, 2005, 06:20:08
Job time : 2.99647 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 9.55124 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-35
Perfect score: 93
Sequence: 1 IIYPGDSDTRYSPSFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	98	1	US-08-478-039-81	Sequence 81, Appl
2	93	100.0	98	1	US-08-476-349A-81	Sequence 81, Appl
3	93	100.0	98	2	US-08-665-202-33	Sequence 33, Appl
4	93	100.0	98	4	US-09-315-574-33	Sequence 33, Appl
5	93	100.0	111	4	US-09-726-219A-171	Sequence 171, App
6	93	100.0	117	3	US-08-545-809A-133	Sequence 133, App
7	93	100.0	119	3	US-09-025-769B-26	Sequence 26, Appl
8	93	100.0	119	4	US-09-490-070A-26	Sequence 26, Appl
9	93	100.0	119	4	US-09-490-153-26	Sequence 26, Appl
10	93	100.0	119	4	US-09-490-324-26	Sequence 26, Appl
11	93	100.0	120	3	US-09-025-769B-40	Sequence 40, Appl
12	93	100.0	120	3	US-09-025-769B-67	Sequence 67, Appl
13	93	100.0	120	4	US-09-490-070A-40	Sequence 40, Appl
14	93	100.0	120	4	US-09-490-070A-67	Sequence 67, Appl
15	93	100.0	120	4	US-09-490-153-40	Sequence 40, Appl
16	93	100.0	120	4	US-09-490-153-67	Sequence 67, Appl
17	93	100.0	120	4	US-09-490-324-40	Sequence 40, Appl
18	93	100.0	120	4	US-09-490-324-67	Sequence 67, Appl
19	88	94.6	122	3	US-08-983-607-30	Sequence 30, Appl
20	88	94.6	125	2	US-08-665-202-44	Sequence 44, Appl
21	88	94.6	125	2	US-08-665-202-45	Sequence 45, Appl
22	88	94.6	125	2	US-08-665-202-46	Sequence 46, Appl
23	88	94.6	125	2	US-08-665-202-47	Sequence 47, Appl
24	88	94.6	125	2	US-08-665-202-48	Sequence 48, Appl
25	88	94.6	125	2	US-08-665-202-49	Sequence 49, Appl
26	88	94.6	125	2	US-08-665-202-50	Sequence 50, Appl
27	88	94.6	125	2	US-08-665-202-51	Sequence 51, Appl
28	88	94.6	125	2	US-08-665-202-52	Sequence 52, Appl
29	88	94.6	125	2	US-08-665-202-53	Sequence 53, Appl
30	88	94.6	125	2	US-08-665-202-54	Sequence 54, Appl
31	88	94.6	125	2	US-08-665-202-55	Sequence 55, Appl
32	88	94.6	125	2	US-08-665-202-57	Sequence 57, Appl
33	88	94.6	125	2	US-08-665-202-58	Sequence 58, Appl
34	88	94.6	125	4	US-09-315-574-44	Sequence 44, Appl
35	88	94.6	125	4	US-09-315-574-45	Sequence 45, Appl
36	88	94.6	125	4	US-09-315-574-46	Sequence 46, Appl
37	88	94.6	125	4	US-09-315-574-47	Sequence 47, Appl
38	88	94.6	125	4	US-09-315-574-48	Sequence 48, Appl
39	88	94.6	125	4	US-09-315-574-49	Sequence 49, Appl
40	88	94.6	125	4	US-09-315-574-50	Sequence 50, Appl
41	88	94.6	125	4	US-09-315-574-51	Sequence 51, Appl
42	88	94.6	125	4	US-09-315-574-52	Sequence 52, Appl
43	88	94.6	125	4	US-09-315-574-53	Sequence 53, Appl
44	88	94.6	125	4	US-09-315-574-54	Sequence 54, Appl
45	88	94.6	125	4	US-09-315-574-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-08-478-039-81
; Sequence 81, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

no SEQ ID 36

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;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  VH5 consensus
US-08-478-039-81

  Query Match             100.0%;  Score 93;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 2
US-08-476-349A-81
; Sequence 81, Application US/08476349A
; Patent No. 5750105
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,349A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/379,072
;      FILING DATE:  25-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/912,292
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/856,281
;      FILING DATE:  23-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,064
;      FILING DATE:  25-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin Esq., Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-161
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  81:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  VH5 consensus
US-08-476-349A-81

  Query Match             100.0%;  Score 93;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 3
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-33

  Query Match             100.0%;  Score 93;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 4
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
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;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/315,574
;      FILING DATE:  20-MAY-99
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,202
;      FILING DATE:  13-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-315-574-33

  Query Match             100.0%;  Score 93;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 5
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
;  APPLICANT: Cambridge Antibody Technology
;  APPLICANT:  Cambridge Antibody Technology Limited
;  APPLICANT:  Medical Research Council
;  APPLICANT:  McCafferty, John
;  APPLICANT:  Pope, Anthony
;  APPLICANT:  Johnson, Kevin
;  APPLICANT:  Hoogenboom, Hendricus
;  APPLICANT:  Griffiths, Andrew
;  APPLICANT:  Jackson, Ronald
;  APPLICANT:  Holliger, Kasper
;  APPLICANT:  Marks, James
;  APPLICANT:  Clackson, Timothy
;  APPLICANT:  Chiswell, David
;  APPLICANT:  Winter, Gregory
;  APPLICANT:  Bonert, Timothy
;  TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
;  FILE REFERENCE: 213839-00013
;  CURRENT APPLICATION NUMBER: US/09/726,219A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: GB 9015198.6
;  PRIOR FILING DATE: 1990-07-10
;  PRIOR APPLICATION NUMBER: GB 9022845.3
;  PRIOR FILING DATE: 1990-10-19
;  PRIOR APPLICATION NUMBER: GB 9022845.3
;  PRIOR FILING DATE: 1990-10-19
;  PRIOR APPLICATION NUMBER: GB 9024503.6
;  PRIOR FILING DATE: 1990-11-12
;  PRIOR APPLICATION NUMBER: GB 9104744.9
;  PRIOR FILING DATE: 1991-03-06
;  PRIOR APPLICATION NUMBER: GB 9110549.4
;  PRIOR FILING DATE: 1991-05-15
;  PRIOR APPLICATION NUMBER: PCT/GB91/01134
;  PRIOR FILING DATE: 1991-07-10
;  PRIOR APPLICATION NUMBER: US 07/971,857
;  PRIOR FILING DATE: 1993-01-08
;  PRIOR APPLICATION NUMBER: US 08/484,893
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 272
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-726-219A-171

  Query Match             100.0%;  Score 93;  DB 4;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 6
US-08-545-809A-133
; Sequence 133, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,809A
;      FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00603
;      FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06501/004001
```

```
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-542-5070
;       TELEFAX:  617-542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  133:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  117 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-545-809A-133

  Query Match           100.0%;  Score 93;  DB 3;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         69 IIYPGDSDTRYSPSFQG 85


RESULT 7
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;     APPLICANT:  Knappik, Achim
;     APPLICANT:  Pack, Peter
;     APPLICANT:  Ilag, Vic
;     APPLICANT:  Ge, Liming
;     APPLICANT:  Moroney, Simon
;     APPLICANT:  Plueckthun, Andreas
;     TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;     NUMBER OF SEQUENCES:  373
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;       STREET:  1251 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10021
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/025,769B
;       FILING DATE:  18-FEB-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP 95 11 3021.0
;       FILING DATE:  18-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  MORPHO/5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)596-9000
;       TELEFAX:  (212)596-9090
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-025-769B-26

  Query Match           100.0%;  Score 93;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 8
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                       White & McAuliffe
;            STREET: 1666 K Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,070A
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Colin G. Sandercock, Esq.
;            REGISTRATION NUMBER: 31,298
;            REFERENCE/DOCKET NUMBER: 37629-0005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 912-2000
;            TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

  Query Match           100.0%;  Score 93;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 9
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
```

```
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,153
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769B
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

  Query Match             100.0%;  Score 93;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 10
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
;   GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,324
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

  Query Match             100.0%;  Score 93;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 11
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  40:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-40

  Query Match             100.0%;  Score 93;  DB 3;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 12
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-67

  Query Match             100.0%;  Score 93;  DB 3;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 13
US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

  Query Match             100.0%;  Score 93;  DB 4;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 14
US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
```

```
;            STREET: 1666 K Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,070A
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Colin G. Sandercock, Esq.
;            REGISTRATION NUMBER: 31,298
;            REFERENCE/DOCKET NUMBER: 37629-0005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 912-2000
;            TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 67:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 120 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

  Query Match            100.0%;  Score 93;  DB 4;  Length 120;
  Best Local Similarity  100.0%;  Pred. No. 9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 15
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,153
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769B
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 40:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 120 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

  Query Match            100.0%;  Score 93;  DB 4;  Length 120;
  Best Local Similarity  100.0%;  Pred. No. 9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         50 IIYPGDSDTRYSPSFQG 66


Search completed: August 18, 2005, 06:22:54
Job time : 9.55124 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 32.1979 Seconds
(without alignments)
206.752 Million cell updates/sec

Title: US-10-684-957-35
Perfect score: 93
Sequence: 1 IIYPGDSDTRYSPSFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	17	15	US-10-384-060-40	Sequence 40, Appl
2	93	100.0	17	15	US-10-374-932-6	Sequence 6, Appli
3	93	100.0	17	15	US-10-379-741-6	Sequence 6, Appli
4	93	100.0	17	16	US-10-128-520-369	Sequence 369, App
5	93	100.0	17	17	US-10-684-957-35	Sequence 35, Appl
6	93	100.0	17	17	US-10-638-265-95	Sequence 95, Appl
7	93	100.0	17	17	US-10-726-332-55	Sequence 55, Appl
8	93	100.0	17	17	US-10-726-332-73	Sequence 73, Appl
9	93	100.0	17	17	US-10-726-332-88	Sequence 88, Appl
10	93	100.0	17	17	US-10-726-332-91	Sequence 91, Appl
11	93	100.0	17	18	US-10-982-725-6	Sequence 6, Appli
12	93	100.0	82	14	US-10-078-958-5	Sequence 5, Appli
13	93	100.0	98	9	US-09-850-165-89	Sequence 89, Appl
14	93	100.0	98	14	US-10-194-975-45	Sequence 45, Appl
15	93	100.0	98	14	US-10-125-687-16	Sequence 16, Appl
16	93	100.0	98	14	US-10-041-860-6	Sequence 6, Appli
17	93	100.0	98	14	US-10-041-860-301	Sequence 301, App
18	93	100.0	98	14	US-10-041-860-302	Sequence 302, App
19	93	100.0	98	14	US-10-041-860-312	Sequence 312, App
20	93	100.0	98	14	US-10-041-860-314	Sequence 314, App
21	93	100.0	98	14	US-10-041-860-318	Sequence 318, App
22	93	100.0	98	14	US-10-041-860-320	Sequence 320, App
23	93	100.0	98	14	US-10-041-860-336	Sequence 336, App
24	93	100.0	98	14	US-10-041-860-338	Sequence 338, App
25	93	100.0	98	14	US-10-041-860-367	Sequence 367, App
26	93	100.0	98	15	US-10-308-817-88	Sequence 88, Appl
27	93	100.0	98	15	US-10-032-037B-106	Sequence 106, App
28	93	100.0	98	15	US-10-032-037B-107	Sequence 107, App
29	93	100.0	98	15	US-10-032-037B-108	Sequence 108, App
30	93	100.0	98	15	US-10-029-988B-106	Sequence 106, App
31	93	100.0	98	15	US-10-029-988B-107	Sequence 107, App
32	93	100.0	98	15	US-10-029-988B-108	Sequence 108, App
33	93	100.0	98	15	US-10-032-423A-106	Sequence 106, App
34	93	100.0	98	15	US-10-032-423A-107	Sequence 107, App
35	93	100.0	98	15	US-10-032-423A-108	Sequence 108, App
36	93	100.0	98	15	US-10-453-698-88	Sequence 88, Appl
37	93	100.0	98	15	US-10-029-926B-106	Sequence 106, App
38	93	100.0	98	15	US-10-029-926B-107	Sequence 107, App
39	93	100.0	98	15	US-10-029-926B-108	Sequence 108, App
40	93	100.0	98	16	US-10-379-392-53	Sequence 53, Appl
41	93	100.0	98	16	US-10-769-144-30	Sequence 30, Appl
42	93	100.0	98	18	US-10-996-191-16	Sequence 16, Appl
43	93	100.0	109	16	US-10-800-197-144	Sequence 144, App
44	93	100.0	109	16	US-10-800-197-145	Sequence 145, App
45	93	100.0	109	16	US-10-800-197-146	Sequence 146, App

ALIGNMENTS

RESULT 1
US-10-384-060-40
; Sequence 40, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH CDR2 sequence
US-10-384-060-40

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Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17
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RESULT 2
US-10-374-932-6
; Sequence 6, Application US/10374932
; Publication No. US20030235586A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP
; CURRENT APPLICATION NUMBER: US/10/374,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-932-6

Query Match 100.0%; Score 93; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 IIYPGDSDTRYSPSFQG 17
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Db          1 IIYPGDSDTRYSPSFQG 17
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RESULT 3
US-10-379-741-6
; Sequence 6, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP2
; CURRENT APPLICATION NUMBER: US/10/379,741
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-6

Query Match 100.0%; Score 93; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 IIYPGDSDTRYSPSFQG 17
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RESULT 4
US-10-128-520-369
; Sequence 369, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-369

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Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 IIYPGDSDTRYSPSFQG 17
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Db          1 IIYPGDSDTRYSPSFQG 17
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RESULT 5
US-10-684-957-35
; Sequence 35, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-35

Query Match 100.0%; Score 93; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 IIYPGDSDTRYSPSFQG 17
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RESULT 6
US-10-638-265-95
; Sequence 95, Application US/10638265
; Publication No. US20050031614A1

; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-95

Query Match 100.0%; Score 93; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 7
US-10-726-332-55
; Sequence 55, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-55

Query Match 100.0%; Score 93; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
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Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 8
US-10-726-332-73
; Sequence 73, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-73

Query Match 100.0%; Score 93; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
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Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 9
US-10-726-332-88
; Sequence 88, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-88

Query Match 100.0%; Score 93; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 10
US-10-726-332-91
; Sequence 91, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee

```
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-91

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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17


RESULT 11
US-10-982-725-6
; Sequence 6, Application US/10982725
; Publication No. US20050123542A1
; GENERAL INFORMATION:
;  APPLICANT: BEURSKENS, Frank
;  APPLICANT:  SCHUURMAN, Janine
;  APPLICANT:  PARREN, Paul
;  APPLICANT:  PETERSEN, Jorgen
;  APPLICANT:  BAADSGAARD, Ole
;  TITLE OF INVENTION: METHODS FOR TREATING DISORDERS INVOLVING MONOCYTES
;  FILE REFERENCE: AMJ-002
;  CURRENT APPLICATION NUMBER: US/10/982,725
;  CURRENT FILING DATE:  2004-11-04
;  PRIOR APPLICATION NUMBER: 60/518552
;  PRIOR FILING DATE: 2003-11-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-725-6

  Query Match             100.0%;  Score 93;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17


RESULT 12
US-10-078-958-5
; Sequence 5, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-078-958-5

  Query Match             100.0%;  Score 93;  DB 14;  Length 82;
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         34 IIYPGDSDTRYSPSFQG 50


RESULT 13
US-09-850-165-89
; Sequence 89, Application US/09850165
; Patent No. US20020150580A1
; GENERAL INFORMATION:
;  APPLICANT: NEWMAN, ROLAND A.
;  APPLICANT:  HANNA, NABIL
;  APPLICANT:  RAAB, RONALD W.
;  TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
;  FILE REFERENCE: 037003-0280614
;  CURRENT APPLICATION NUMBER: US/09/850,165
;  CURRENT FILING DATE:  2001-05-08
;  PRIOR APPLICATION NUMBER: 09/082,472
;  PRIOR FILING DATE: 1998-05-21
;  PRIOR APPLICATION NUMBER: 08/476,237
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/397,072
;  PRIOR FILING DATE: 1995-04-17
;  PRIOR APPLICATION NUMBER: 07/912,292
;  PRIOR FILING DATE: 1992-07-10
;  PRIOR APPLICATION NUMBER: 07/856,281
;  PRIOR FILING DATE: 1992-03-23
;  PRIOR APPLICATION NUMBER: 07/735,064
;  PRIOR FILING DATE: 1991-07-25
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (19)
;   OTHER INFORMATION: Arg or Lys
US-09-850-165-89

  Query Match             100.0%;  Score 93;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 7e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         50 IIYPGDSDTRYSPSFQG 66


RESULT 14
US-10-194-975-45
; Sequence 45, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
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; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-45

Query Match 100.0%; Score 93; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
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Db 50 IIYPGDSDTRYSPSFQG 66

RESULT 15
US-10-125-687-16
; Sequence 16, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-687-16

Query Match 100.0%; Score 93; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 50 IIYPGDSDTRYSPSFQG 66

Search completed: August 18, 2005, 07:08:03
Job time : 32.3229 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 36.6431 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-35
Perfect score: 93
Sequence: 1 IIYPGDSDTRYSPSFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	17	6	ABR01560	Abr01560 Human ant
2	93	100.0	17	6	ABU08151	Abu08151 ErbB2 rec
3	93	100.0	17	7	ADD69218	Add69218 Human hea
4	93	100.0	17	7	ADD69224	Add69224 Human hea
5	93	100.0	17	7	ADD69221	Add69221 Human hea
6	93	100.0	17	7	ADD69227	Add69227 Human hea
7	93	100.0	17	7	ADD69230	Add69230 Human hea
8	93	100.0	17	8	ADH89396	Adh89396 Human tra
9	93	100.0	17	8	ADP47140	Adp47140 Human pho
10	93	100.0	17	8	ADP47176	Adp47176 Human pho
11	93	100.0	17	8	ADP47158	Adp47158 Human pho
12	93	100.0	17	8	ADP47173	Adp47173 Human pho
13	93	100.0	17	8	ADS87942	Ads87942 Anti-IFN-
14	93	100.0	17	8	ADS94939	Ads94939 Anti-IFN-
15	93	100.0	17	8	ADR69906	Adr69906 Human IL-
16	93	100.0	84	2	AAW62797	Aaw62797 Amino aci
17	93	100.0	98	2	AAW54008	Aaw54008 Human Ant
18	93	100.0	98	5	ABG78233	Abg78233 Human Fv
19	93	100.0	98	5	ABG78231	Abg78231 Human Fv
20	93	100.0	98	5	ABG78232	Abg78232 Human Fv
21	93	100.0	98	5	ABG91924	Abg91924 Human ant
22	93	100.0	98	5	ABG91922	Abg91922 Human ant
23	93	100.0	98	5	ABG91923	Abg91923 Human ant
24	93	100.0	98	6	ABU56809	Abu56809 Human Imm
25	93	100.0	98	6	ABP56508	Abp56508 Human ant
26	93	100.0	98	6	ABJ18687	Abj18687 Antibody
27	93	100.0	98	6	ABO27112	Abo27112 Human ger
28	93	100.0	98	7	ADD69247	Add69247 Human hea
29	93	100.0	98	7	ADF10156	Adf10156 Antibody
30	93	100.0	98	7	ADF09948	Adf09948 Antibody
31	93	100.0	98	7	ADF10053	Adf10053 VEGF anti
32	93	100.0	98	7	ADK18943	Adk18943 Anti-huma
33	93	100.0	98	7	ADK18888	Adk18888 Anti-huma
34	93	100.0	98	7	ADK18877	Adk18877 Anti-huma
35	93	100.0	98	7	ADK18878	Adk18878 Anti-huma
36	93	100.0	98	7	ADK18912	Adk18912 Anti-huma
37	93	100.0	98	7	ADK18582	Adk18582 Anti-huma
38	93	100.0	98	7	ADK18890	Adk18890 Anti-huma
39	93	100.0	98	7	ADK18896	Adk18896 Anti-huma
40	93	100.0	98	7	ADK18894	Adk18894 Anti-huma
41	93	100.0	98	7	ADK18914	Adk18914 Anti-huma
42	93	100.0	98	7	ADJ80328	Adj80328 VH gene 1
43	93	100.0	98	8	ADR46847	Adr46847 Human VH5
44	93	100.0	109	8	ADI05782	Adi05782 Human mon
45	93	100.0	109	8	ADP22377	Adp22377 Human ant

ALIGNMENTS

RESULT 1
ABR01560
ID ABR01560 standard; peptide; 17 AA.
XX
AC ABR01560;
XX
DT 16-APR-2003 (first entry)
XX
DE Human anti-TIMP-1 Fab VLCDR3 #48.
XX
KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
KW variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;
KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
XX
OS Homo sapiens.
XX
PN WO200286085-A2.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-US012801.
XX
PR 24-APR-2001; 2001US-0285683P.
XX
PA (FARB) BAYER CORP.
PA (MORP-) MORPHOSYS AG.
XX
PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
XX
DR WPI; 2003-129114/12.
XX
PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.
XX
PS Claim 17; Page 226; 228pp; English.
XX
CC The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)
CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP
CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
CC variable light chain (VLC)DR3 region. An antibody preparation of the
CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
CC activity. The human antibody is useful for decreasing an MMP-inhibiting

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CC   activity of a TIMP-1. It is especially useful for ameliorating the
CC   symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
CC   alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
CC   nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
CC   fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
CC   antibody is also useful for detecting a TIMP-1 in a test preparation, or
CC   in diagnosing a disorder in which a TIMP-1 level is elevated. The
CC   sequences shown in ABR01407-ABR01449 and ABR01555-ABR01569 represent
CC   VLCDR regions of an antibody of the invention
XX
SQ   Sequence 17 AA;

  Query Match            100.0%;  Score 93;  DB 6;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17


RESULT 2
ABU08151
ID   ABU08151 standard; peptide; 17 AA.
XX
AC   ABU08151;
XX
DT   10-MAY-2003  (first entry)
XX
DE   ErbB2 receptor antibody VH domain CDR-2.
XX
KW   Human; single-chain antibody; anti-ErbB2 antibody; Erbicin;
KW   growth inhibitor; ErbB2 receptor; transmembrane tyrosine kinase receptor;
KW   RTK; antibody; gene therapy; bacteriophage; antitumour agent; tumour;
KW   mammary carcinoma; ovarian carcinoma; colon carcinoma; lung carcinoma;
KW   salivary gland tumour; gastric tumour; antiproliferative; cytostatic; VH;
KW   CDR; complementarity determining region; variable domain; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2003006509-A2.
XX
PD   23-JAN-2003.
XX
PF   10-JUL-2002; 2002WO-EP007671.
XX
PR   10-JUL-2001; 2001IT-RM000408.
XX
PA   (UYNA-) UNIV NAPOLI STUDI FEDERICO II.
XX
PI   D'alessio G,  Piccoli R,  De Lorenzo C,  Palmer DB,  Ritter MA;
XX
DR   WPI; 2003-221720/21.
DR   N-PSDB; ABX12974.
XX
PT   New recombinant single-chain anti-ErbB2 antibody of human origin, useful
PT   for pharmaceutical and diagnostic use, and as an antitumor agent for
PT   mammary, ovarian, colon, lung carcinomas, salivary gland or gastric
PT   tumors.
XX
PS   Claim 10; Page 8; 47pp; English.
XX
CC   The invention discloses a recombinant single-chain anti-ErbB2 antibody of
CC   human origin able to inhibit growth of cells expressing the ErbB2
CC   receptor, referred to as Erbicin. The ErbB2 transmembrane tyrosine kinase
CC   receptor (RTK) is highly expressed in breast, ovary and lung carcinomas
CC   as well as salivary gland or gastric tumours. The antibodies, new
CC   proteins, nucleotide sequences (gene therapy) and bacteriophage are
CC   useful for pharmaceutical and diagnostic use, and as an antitumour agent,
CC   where the tumour can be mammary, ovarian, colon, lung carcinomas,
CC   salivary gland or gastric tumours. They are also useful in preparing
CC   antiproliferative and antitumour drugs. The sequences presented are the
CC   nucleic acids and encoded polypeptides that were used in the invention to
CC   create the antibody
XX
SQ   Sequence 17 AA;

  Query Match            100.0%;  Score 93;  DB 6;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17


RESULT 3
ADD69218
ID   ADD69218 standard; peptide; 17 AA.
XX
AC   ADD69218;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human heavy chain variable region CDR2 peptide - SEQ ID 22.
XX
KW   monoclonal antibody; heavy chain variable region; light; framework;
KW   complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW   prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW   colon cancer; renal carcinoma; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO2003064606-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-US002448.
XX
PR   28-JAN-2002; 2002US-00059989.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Deo YM,  Graziano R,  Hudson D,  Holmes EH,  Tino WT,  Black A;
XX
DR   WPI; 2003-618360/58.
XX
PT   New isolated human monoclonal antibody comprising a human heavy chain and
PT   a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT   CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT   cancer.
XX
PS   Claim 2; SEQ ID NO 22; 136pp; English.
XX
CC   The invention relates to a novel isolated human monoclonal antibody
CC   comprising a human heavy chain variable region and a human light chain
CC   variable region both comprising FR (framework region)-1, CDR
CC   (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC   sequences. The antibody is directed against the human prostate specific
CC   membrane antigen (PSMA). The monoclonal antibody of the invention
CC   demonstrates cytostatic activity and may be useful for treating or
CC   preventing a disease characterised by the growth of tumour cells such as
CC   cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC   well as duing gene therapy procedures. The current sequence is that of
CC   the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ   Sequence 17 AA;

  Query Match            100.0%;  Score 93;  DB 7;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17
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```
RESULT 4
ADD69224
ID   ADD69224 standard; peptide; 17 AA.
XX
AC   ADD69224;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human heavy chain variable region CDR2 peptide - SEQ ID 28.
XX
KW   monoclonal antibody; heavy chain variable region; light; framework;
KW   complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW   prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW   colon cancer; renal carcinoma; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO2003064606-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-US002448.
XX
PR   28-JAN-2002; 2002US-00059989.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Deo YM,  Graziano R,  Hudson D,  Holmes EH,  Tino WT,  Black A;
XX
DR   WPI; 2003-618360/58.
XX
PT   New isolated human monoclonal antibody comprising a human heavy chain and
PT   a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT   CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT   cancer.
XX
PS   Claim 2; SEQ ID NO 28; 136pp; English.
XX
CC   The invention relates to a novel isolated human monoclonal antibody
CC   comprising a human heavy chain variable region and a human light chain
CC   variable region both comprising FR (framework region)-1, CDR
CC   (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC   sequences. The antibody is directed against the human prostate specific
CC   membrane antigen (PSMA). The monoclonal antibody of the invention
CC   demonstrates cytostatic activity and may be useful for treating or
CC   preventing a disease characterised by the growth of tumour cells such as
CC   cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC   well as duing gene therapy procedures. The current sequence is that of
CC   the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ   Sequence 17 AA;

  Query Match             100.0%;  Score 93;  DB 7;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17


RESULT 5
ADD69221
ID   ADD69221 standard; peptide; 17 AA.
XX
AC   ADD69221;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human heavy chain variable region CDR2 peptide - SEQ ID 25.
XX
KW   monoclonal antibody; heavy chain variable region; light; framework;
KW   complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW   prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW   colon cancer; renal carcinoma; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO2003064606-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-US002448.
XX
PR   28-JAN-2002; 2002US-00059989.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Deo YM,  Graziano R,  Hudson D,  Holmes EH,  Tino WT,  Black A;
XX
DR   WPI; 2003-618360/58.
XX
PT   New isolated human monoclonal antibody comprising a human heavy chain and
PT   a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT   CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT   cancer.
XX
PS   Claim 2; SEQ ID NO 25; 136pp; English.
XX
CC   The invention relates to a novel isolated human monoclonal antibody
CC   comprising a human heavy chain variable region and a human light chain
CC   variable region both comprising FR (framework region)-1, CDR
CC   (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC   sequences. The antibody is directed against the human prostate specific
CC   membrane antigen (PSMA). The monoclonal antibody of the invention
CC   demonstrates cytostatic activity and may be useful for treating or
CC   preventing a disease characterised by the growth of tumour cells such as
CC   cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC   well as duing gene therapy procedures. The current sequence is that of
CC   the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ   Sequence 17 AA;

  Query Match             100.0%;  Score 93;  DB 7;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db          1 IIYPGDSDTRYSPSFQG 17


RESULT 6
ADD69227
ID   ADD69227 standard; peptide; 17 AA.
XX
AC   ADD69227;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human heavy chain variable region CDR2 peptide - SEQ ID 31.
XX
KW   monoclonal antibody; heavy chain variable region; light; framework;
KW   complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW   prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW   colon cancer; renal carcinoma; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO2003064606-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-US002448.
XX
```

PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 31; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as duing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
|||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 7
ADD69230
ID ADD69230 standard; peptide; 17 AA.
XX
AC ADD69230;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heavy chain variable region CDR2 peptide - SEQ ID 34.
XX
KW monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CRD3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 34; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CRD3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as duing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
|||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 8
ADH89396
ID ADH89396 standard; peptide; 17 AA.
XX
AC ADH89396;
XX
DT 15-APR-2004 (first entry)
XX
DE Human transferrin fusion protein-related CDR2 peptide SeqID40.
XX
KW fusion protein; transferrin protein; glycosylation;
KW antibody variable region; cytostatic; antibacterial; virucide;
KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
KW viral infection; parasitic infection; neoplasm; autoimmune disease;
KW arthritis; graft rejection.
XX
OS Unidentified.
XX
PN US2003226155-A1.
XX
PD 04-DEC-2003.
XX
PF 10-MAR-2003; 2003US-00384060.
XX
PR 30-AUG-2001; 2001US-0315745P.
PR 30-NOV-2001; 2001US-0334059P.
PR 30-AUG-2002; 2002US-00231494.
PR 30-AUG-2002; 2002US-0406977P.
XX
PA (BIOR-) BIOREXIS PHARM CORP.
XX
PI Sadeghi H, Prior CP, Turner A;
XX
DR WPI; 2004-022093/02.
XX
PT New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.
XX
PS Example 2; SEQ ID NO 40; 82pp; English.
XX
CC This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,

CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a CDR 2 peptide which was used in the exemplification
CC of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 9
ADP47140
ID ADP47140 standard; peptide; 17 AA.
XX
AC ADP47140;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb heavy chain peptide #5.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 55; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC heavy chain peptide.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 10
ADP47176
ID ADP47176 standard; peptide; 17 AA.
XX
AC ADP47176;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb heavy chain peptide #41.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 91; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC heavy chain peptide.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 11
ADP47158
ID ADP47158 standard; peptide; 17 AA.
XX
AC ADP47158;

XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb heavy chain peptide #23.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 73; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC heavy chain peptide.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
|||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 12
ADP47173
ID ADP47173 standard; peptide; 17 AA.
XX
AC ADP47173;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific mAb heavy chain peptide #38.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 88; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents a human PLA2-specific monoclonal antibody
CC heavy chain peptide.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
|||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 13
ADS87942
ID ADS87942 standard; peptide; 17 AA.
XX
AC ADS87942;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR2 SEQ ID NO:35.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX

PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 22; SEQ ID NO 35; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
|||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 14
ADS94939
ID ADS94939 standard; peptide; 17 AA.
XX
AC ADS94939;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR2 SEQ ID NO:35.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 4; SEQ ID NO 35; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
|||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

RESULT 15
ADR69906
ID ADR69906 standard; peptide; 17 AA.
XX
AC ADR69906;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human IL-15 monoclonal antibody VH-region CDR2 SEQ ID NO:6.
XX
KW monoclonal antibody; heavy chain variable region; interleukin-15; IL-15;
KW antiarthritic; ophthalmological; neuroprotective; nootropic;
KW gastrointestinal; hepatotropic; antiallergic; haemostatic;
KW dermatological; respiratory; cytostatic; immunosuppressive; vasotropic;
KW gynaecological; antimicrobial; CDR.
XX
OS Homo sapiens.
XX
PN WO2004076620-A2.
XX
PD 10-SEP-2004.
XX
PF 25-FEB-2004; 2004WO-IB000484.
XX
PR 26-FEB-2003; 2003US-00374932.
PR 05-MAR-2003; 2003US-00379741.

XX
PA (GENM-) GENMAB AS.
XX
PI Van De Winkel JGJ, Van Dijk MA, Schuurman J, Gerritsen AF;
PI Baadsgaard ODMS, Petersen J;
XX
DR WPI; 2004-653391/63.
XX
PT New isolated human monoclonal antibody that specifically binds to human
PT IL-15, useful for diagnosing, preventing or treating lupus, ulcerative
PT colitis, allograft rejection and graft-versus-host disease.
XX
PS Claim 1; SEQ ID NO 6; 116pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody which
CC specifically binds to human interleukin-15 (IL-15) comprising at least
CC one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
CC amino acids (ADR69905-ADR69910, respectively), a sequence at least 90,
CC 95, 98 or 99% homologous to the amino acid sequences, or their fragments,
CC which retain the ability to specifically bind to human IL-15. A
CC monoclonal antibody of the invention has antiarthritic, ophthalmological,
CC neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
CC haemostatic, dermatological, respiratory, cytostatic, immunosuppressive,
CC vasotropic, gynaecological, and antimicrobial activity. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of conditions associated with aberrant expression or
CC activity of the IL-15, such as arthritis, connective tissue disorders,
CC ophthalmological disorders, neurological disorders, gastrointestinal and
CC hepatic disorders, allergic disorders, haematologic disorders, allergic
CC disorders, skin disorders, pulmonary disorders, malignancies,
CC transplantation-derived disorders, endocrinological disorders, vascular
CC disorders, gynaecological disorders and infectious diseases, including
CC ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
CC allograft rejection and graft-versus-host disease. The present sequence
CC represents CDR2 of the heavy chain variable (VH) region of a human IL-15
CC monoclonal antibody of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||
Db 1 IIYPGDSDTRYSPSFQG 17

Search completed: August 18, 2005, 06:09:14
Job time : 37.6431 secs

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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 6.78799 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-35
Perfect score: 93
Sequence: 1 IIYPGDSDTRYSPSFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	98	2	PH1274	Ig heavy chain V r
2	93	100.0	98	2	S26907	Ig heavy chain V r
3	93	100.0	101	2	S12428	Ig heavy chain V r
4	93	100.0	101	2	S12424	Ig heavy chain V r
5	93	100.0	102	2	PH1266	Ig heavy chain V r
6	93	100.0	102	2	PH1279	Ig heavy chain V r
7	93	100.0	102	2	PH1281	Ig heavy chain V r
8	93	100.0	102	2	PH1277	Ig heavy chain V r
9	93	100.0	102	2	PH1244	Ig heavy chain V r
10	93	100.0	102	2	PH1267	Ig heavy chain V r
11	93	100.0	102	2	PH1272	Ig heavy chain V r
12	93	100.0	102	2	PH1282	Ig heavy chain V r
13	93	100.0	102	2	PH1248	Ig heavy chain V r
14	93	100.0	102	2	PH1280	Ig heavy chain V r
15	93	100.0	102	2	PH1258	Ig heavy chain V r
16	93	100.0	102	2	PH1264	Ig heavy chain V r
17	93	100.0	102	2	PH1259	Ig heavy chain V r
18	93	100.0	102	2	PH1273	Ig heavy chain V r
19	93	100.0	102	2	PH1249	Ig heavy chain V r
20	93	100.0	102	2	PH1271	Ig heavy chain V r
21	93	100.0	102	2	PH1278	Ig heavy chain V r
22	93	100.0	104	2	B36006	Ig heavy chain V r
23	93	100.0	113	2	PH1428	Ig heavy chain V r
24	93	100.0	115	2	PH1557	Ig heavy chain V r
25	93	100.0	117	2	A28846	Ig heavy chain pre
26	93	100.0	117	2	S19670	Ig heavy chain V r
27	93	100.0	123	2	PH1423	Ig heavy chain V r
28	93	100.0	123	2	S38492	Ig heavy chain - h
29	93	100.0	123	2	C36006	Ig heavy chain V r
30	93	100.0	127	2	PH1414	Ig heavy chain V r
31	93	100.0	127	2	PH1409	Ig heavy chain V r
32	93	100.0	128	2	S16685	Ig heavy chain V r
33	93	100.0	134	2	PH1422	Ig heavy chain V r
34	93	100.0	136	2	A49047	Ig heavy chain V r
35	93	100.0	136	2	PH1559	Ig heavy chain V r
36	93	100.0	139	2	PH1558	Ig heavy chain V r
37	90	96.8	102	2	PH1252	Ig heavy chain V r
38	90	96.8	127	2	PH1411	Ig heavy chain V r
39	89	95.7	102	2	PH1247	Ig heavy chain V r
40	89	95.7	123	2	PH1413	Ig heavy chain V r
41	88	94.6	86	2	S12580	Ig heavy chain V r
42	88	94.6	102	2	PH1265	Ig heavy chain V r
43	88	94.6	119	2	S36257	Ig heavy chain V r
44	87	93.5	127	2	PH1420	Ig heavy chain V r
45	87	93.5	127	2	PH1415	Ig heavy chain V r

ALIGNMENTS

RESULT 1
PH1274
Ig heavy chain V region (clone PBL5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1274
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1274
A;Molecule type: DNA
A;Residues: 1-98 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 93; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70
```

RESULT 2
S26907
Ig heavy chain V region (DP-73) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26907
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26907
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12373; NID:g32965; PIDN:CAA78243.1; PID:g32966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         50 IIYPGDSDTRYSPSFQG 66
```

```
RESULT 3
S12428
Ig heavy chain V region (5JB) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S12428
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12428
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56367
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         53 IIYPGDSDTRYSPSFQG 69


RESULT 4
S12424
Ig heavy chain V region (5) - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C;Accession: S12424; S12425; S12426; S12427; S12429; S12432
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12424
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SAN>
A;Cross-references: EMBL:X56372
A;Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
A;Accession: S12425
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA2>
A;Cross-references: EMBL:X56373
A;Accession: S12426
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA3>
A;Cross-references: EMBL:X56370
A;Accession: S12427
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA4>
A;Cross-references: EMBL:X56368
A;Accession: S12429
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA5>
A;Cross-references: EMBL:X56369
A;Accession: S12432
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-101 <SA6>
A;Cross-references: EMBL:X56371
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         53 IIYPGDSDTRYSPSFQG 69


RESULT 5
PH1266
Ig heavy chain V region (clone VERG5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1266
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chroni
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1266
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70


RESULT 6
PH1279
Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-J
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1279
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1279
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70


RESULT 7
PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1281
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
```

A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1281
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 54 IIYPGDSDTRYSPSFQG 70

RESULT 8
PH1277
Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 54 IIYPGDSDTRYSPSFQG 70

RESULT 9
PH1244
Ig heavy chain V region (clone CORD2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1244
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1244
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 54 IIYPGDSDTRYSPSFQG 70

RESULT 10
PH1267
Ig heavy chain V region (clone VERG9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1267
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1267
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 54 IIYPGDSDTRYSPSFQG 70

RESULT 11
PH1272
Ig heavy chain V region (clone PBL3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1272
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1272
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTRYSPSFQG 17
||||||||||||||||||
Db 54 IIYPGDSDTRYSPSFQG 70

RESULT 12
PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 102;

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  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70


RESULT 13
PH1248
Ig heavy chain V region (clone CORD6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1248
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1248
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70


RESULT 14
PH1280
Ig heavy chain V region (clone PBL11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1280
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1280
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70


RESULT 15
PH1258
Ig heavy chain V region (clone CD-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1258
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1258
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: cord blood B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 93;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IIYPGDSDTRYSPSFQG 17
              |||||||||||||||||
Db         54 IIYPGDSDTRYSPSFQG 70


Search completed: August 18, 2005, 06:20:09
Job time : 7.78799 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 31.8975 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-35
Perfect score: 93
Sequence: 1 IIYPGDSDTRYSPSFQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	67.7	474	2	Q8R3H6	mus musculu
2	60	64.5	111	2	Q9D9B8	Q9d9b8 mus musculu
3	60	64.5	118	2	Q9Z1C4	Q9z1c4 mus musculu
4	59	63.4	614	2	Q7TMT6	Q7tmt6 mus musculu
5	58	62.4	481	2	Q91WT1	Q91wt1 mus musculu
6	57	61.3	117	1	HV52_MOUSE	P06327 mus musculu
7	54	58.1	117	1	HV06_MOUSE	P01750 mus musculu
8	53	57.0	110	2	Q9JL83	Q9jl83 mus musculu
9	51	54.8	463	2	Q99LC4	Q99lc4 mus musculu
10	49	52.7	117	1	HV05_MOUSE	P01749 mus musculu
11	48	51.6	909	2	Q6WJ05	Q6wj05 gossypium h
12	47	50.5	147	2	Q925S3	Q925s3 mus musculu
13	47	50.5	330	2	Q93KW0	Q93kw0 streptomyce
14	46	49.5	155	2	O65840	O65840 linum usita
15	46	49.5	234	2	Q9ZB85	Q9zb85 burkholderi
16	46	49.5	256	2	Q88JC2	Q88jc2 pseudomonas
17	46	49.5	464	2	Q6PF95	Q6pf95 mus musculu
18	46	49.5	518	2	Q8BDG3	Q8bdg3 bovine papi
19	46	49.5	1335	2	Q9BL05	Q9bl05 caenorhabdi
20	46	49.5	1459	2	Q977Z6	Q977z6 thermoplasm
21	45	48.4	68	2	O51816	O51816 treponema p
22	45	48.4	152	2	Q8B571	Q8b571 pseudocowpo
23	45	48.4	243	2	Q51582	Q51582 plectonema
24	45	48.4	251	2	Q9U7J4	Q9u7j4 plasmodium
25	45	48.4	430	2	O52724	O52724 treponema p
26	45	48.4	430	2	O52725	O52725 treponema p
27	45	48.4	430	2	O52726	O52726 treponema p
28	45	48.4	562	2	O52722	O52722 treponema p
29	45	48.4	568	2	O52723	O52723 treponema p
30	45	48.4	596	2	Q9K2N7	Q9k2n7 treponema p
31	45	48.4	596	2	Q9L814	Q9l814 treponema p
32	45	48.4	598	2	Q6PNG6	Q6png6 treponema p
33	45	48.4	598	2	Q6QAI7	Q6qai7 treponema p
34	45	48.4	598	2	Q6QAI8	Q6qai8 treponema p
35	45	48.4	598	2	Q6QH97	Q6qh97 treponema p
36	45	48.4	598	2	Q6QH98	Q6qh98 treponema p
37	45	48.4	598	2	Q7BN66	Q7bn66 treponema p
38	45	48.4	598	2	Q9L815	Q9l815 treponema p
39	45	48.4	598	2	O88138	O88138 treponema p
40	45	48.4	609	2	Q6QMH3	Q6qmh3 treponema p
41	45	48.4	609	2	O83629	O83629 treponema p
42	45	48.4	1036	2	O86999	O86999 clostridium
43	45	48.4	2203	2	Q8I2C4	Q8i2c4 plasmodium
44	45	48.4	4543	1	LRP1_CHICK	P98157 gallus gall
45	44	47.3	136	2	Q7TPE3	Q7tpe3 mus musculu

ALIGNMENTS

RESULT 1
Q8R3H6
ID Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AU044919 protein.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR HSSP; P01869; 1CL7.
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 4.

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DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

  Query Match           67.7%;  Score 63;  DB 2;  Length 474;
  Best Local Similarity   68.8%;  Pred. No. 0.066;
  Matches   11;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              |:||| || ||  |||
Db         70 IFPGDGDTHYSGKFQG 85


RESULT 2
Q9D9B8
ID   Q9D9B8      PRELIMINARY;      PRT;   111 AA.
AC   Q9D9B8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE   library, clone:1700110L11 product:immunoglobulin heavy chain 6 (heavy
DE   chain of IgM), full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK007163; BAB24877.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   111 AA;  11976 MW;  874DDF7BD98BD7B2 CRC64;

  Query Match           64.5%;  Score 60;  DB 2;  Length 111;
  Best Local Similarity   62.5%;  Pred. No. 0.039;
  Matches   10;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              ||||| || |:  |:|
Db         57 IYPGDGDTNYNGKFKG 72


RESULT 3
Q9Z1C4
ID   Q9Z1C4      PRELIMINARY;      PRT;   118 AA.
AC   Q9Z1C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/c;
RX   MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.A., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Mol. Immunol. 34:441-452(1997).
DR   EMBL; U78801; AAD00293.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;

  Query Match           64.5%;  Score 60;  DB 2;  Length 118;
  Best Local Similarity   62.5%;  Pred. No. 0.042;
  Matches   10;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              ||||| || |:  |:|
Db         51 IYPGDGDTSYTQKFRG 66


RESULT 4
Q7TMT6
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```
ID   Q7TMT6      PRELIMINARY;      PRT;   614 AA.
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MGC60843 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053409; AAH53409.1; -.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   614 AA;  67746 MW;  839BAF3B8D124F89 CRC64;

  Query Match             63.4%;  Score 59;  DB 2;  Length 614;
  Best Local Similarity   56.2%;  Pred. No. 0.42;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              :|||| || |:  |:|
Db         70 VYPGDGDTNYNGKFKG 85


RESULT 5
Q91WT1
ID   Q91WT1      PRELIMINARY;      PRT;   481 AA.
AC   Q91WT1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013490; AAH13490.1; -.
DR   HSSP; P01751; 1A6W.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   481 AA;  52105 MW;  97DF68D159463F65 CRC64;

  Query Match             62.4%;  Score 58;  DB 2;  Length 481;
  Best Local Similarity   56.2%;  Pred. No. 0.47;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              |||||  :|:|:  |:|
Db         70 IYPGDGNTKYNEKFKG 85


RESULT 6
HV52_MOUSE
ID   HV52_MOUSE      STANDARD;      PRT;   117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558 A1/A4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
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DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V region VH558 A1/A4.
FT   DOMAIN       20     49       Framework-1.
FT   DOMAIN       50     54       Complementarity-determining-1.
FT   DOMAIN       55     68       Framework-2.
FT   DOMAIN       69     85       Complementarity-determining-2.
FT   DOMAIN       86    117       Framework-3.
FT   DISULFID     41    115       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;

  Query Match             61.3%;  Score 57;  DB 1;  Length 117;
  Best Local Similarity   56.2%;  Pred. No. 0.13;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              |||||  |:|:  |:|
Db         70 IYPGDGSTKYNEKFKG 85


RESULT 7
HV06_MOUSE
ID   HV06_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region 102 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: This germline gene belongs to a set of closely
CC       related genes that could encode V regions of NPb antibodies.
DR   PIR; A02032; HVMS02.
DR   PDB; 1QNZ; NMR; H=20-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V region 102.
FT   DOMAIN       20     49       Framework-1.
FT   DOMAIN       50     54       Complementarity-determining-1.
FT   DOMAIN       55     68       Framework-2.
FT   DOMAIN       69     85       Complementarity-determining-2.
FT   DOMAIN       86    117       Framework-3.
FT   DISULFID     41    115       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12867 MW;  740A65DD851FCA8C CRC64;

  Query Match             58.1%;  Score 54;  DB 1;  Length 117;
  Best Local Similarity   56.2%;  Pred. No. 0.43;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              |:| |||| |:  |:|
Db         70 IHPSDSDTNYNQKFKG 85


RESULT 8
Q9JL83
ID   Q9JL83      PRELIMINARY;      PRT;   110 AA.
AC   Q9JL83;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RX   DOI=10.1128/IAI.68.10.5803-5808.2000;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206023; AAF69321.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     110    110
SQ   SEQUENCE   110 AA;  12052 MW;  84E6F2AD219AF95E CRC64;

  Query Match             57.0%;  Score 53;  DB 2;  Length 110;
  Best Local Similarity   56.2%;  Pred. No. 0.59;
  Matches    9;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              ||||| |   |:  |:|
Db         43 IYPGDGDAYYNGKFKG 58


RESULT 9
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-4 protein.
GN   Name=Igh-4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   PIR; B45837; B45837.
DR   HSSP; P01869; 1CL7.
DR   MGD; MGI:96446; Igh-4.
DR   GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR   GO; GO:0003823; F:antigen binding; IDA.
DR   GO; GO:0019733; P:antibacterial humoral response (sensu Verte. . .; IDA.
DR   GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR   GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR   GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR   GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR   GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR   GO; GO:0050778; P:positive regulation of immune response; IDA.
DR   GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR   GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR   GO; GO:0001798; P:positive regulation of type IIa hypersensit. . .; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

  Query Match           54.8%;  Score 51;  DB 2;  Length 463;
  Best Local Similarity 56.2%;  Pred. No. 6.8;
  Matches    9;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              ||||  :| ||  |:|
Db         70 IYPGSGNTYYSEKFKG 85


RESULT 10
HV05_MOUSE
ID   HV05_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01749;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V region 3 precursor.
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: This germline gene belongs to a set of closely
CC       related genes that could encode V regions of NPb antibodies.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00536; AAA38605.1; -.
DR   PIR; A02031; HVMS3.
DR   HSSP; P01810; 2FBJ.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V region 3.
FT   DOMAIN       20     49       Framework-1.
FT   DOMAIN       50     54       Complementarity-determining-1.
FT   DOMAIN       55     68       Framework-2.
FT   DOMAIN       69     85       Complementarity-determining-2.
FT   DOMAIN       86    117       Framework-3.
FT   DISULFID     41    115       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13016 MW;  427C861C53975EDC CRC64;

  Query Match           52.7%;  Score 49;  DB 1;  Length 117;
  Best Local Similarity 53.3%;  Pred. No. 3;
  Matches    8;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQ 16
              ||| ||:| |:  |:
Db         70 IYPSDSETHYNQKFK 84


RESULT 11
Q6WJ05
ID   Q6WJ05      PRELIMINARY;      PRT;   909 AA.
AC   Q6WJ05;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Central motor kinesin 1.
GN   Name=CMK1;
OS   Gossypium hirsutum (Upland cotton).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX   NCBI_TaxID=3635;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lu L., Lee Y.-R.J., Pan R., Liu B.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY283056; AAQ18797.1; -.
DR   GO; GO:0005875; C:microtubule associated complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003774; F:motor activity; IEA.
DR   InterPro; IPR001752; kinesin_motor.
DR   Pfam; PF00225; Kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   ATP-binding; Microtubule; Motor protein.
SQ   SEQUENCE   909 AA;  100814 MW;  424E3C6DF67EDF4F CRC64;
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  Best Local Similarity   64.3%;  Pred. No. 48;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 PGDSDTRYSPSFQG 17
              || ||  ||| |:|
Db        115 PGTSDGFYSPEFRG 128


RESULT 12
Q925S3
ID   Q925S3      PRELIMINARY;      PRT;   147 AA.
AC   Q925S3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MRP3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   PubMed=11819679;
RA   Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA   Su C.;
RT   "Mechanism of exogenous nucleic acids and their precursors improving
RT   the repair of intestinal epithelium after irradiation in mice.";
RL   World J. Gastroenterol. 6:709-717(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Cui D., Zeng G., Yan X., Li X., Su C.;
RT   "Cloning of mouse genes related to repairing of intestinal epithelium
RT   of the irradiated mice by treatment with the intestinal RNA of mice of
RT   the same strain.";
RL   Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR   EMBL; AF240166; AAK43731.1; -.
DR   HSSP; P01751; 1A6W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   147 AA;  16274 MW;  800594A12B97191F CRC64;

  Query Match             50.5%;  Score 47;  DB 2;  Length 147;
  Best Local Similarity   43.8%;  Pred. No. 8.5;
  Matches    7;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              |:||:  | |:  |:|
Db         53 IFPGEGSTEYNEKFKG 68


RESULT 13
Q93KW0
ID   Q93KW0      PRELIMINARY;      PRT;   330 AA.
AC   Q93KW0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative oxidoreductase.
GN   Name=aviZ1;
OS   Streptomyces viridochromogenes.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1938;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Tue57;
RX   MEDLINE=21303144; PubMed=11410376; DOI=10.1016/S1074-5521(01)00040-0;
RA   Weitnauer G., Muhlenweg A., Trefzer A., Hoffmeister D., Sussmuth R.D.,
RA   Jung G., Welzel K., Vente A., Girreser U., Bechthold A.;
RT   "Biosynthesis of the orthosomycin antibiotic avilamycin A: deductions
RT   from the molecular analysis of the avi biosynthetic gene cluster of
RT   Streptomyces viridochromogenes Tu57 and production of new
RT   antibiotics.";
RL   Chem. Biol. 8:569-581(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Tue57;
RA   Mosbacher T., Weitnauer G., Bechthold A., Schulz G.E.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF333038; AAK83185.1; -.
DR   HSSP; Q46857; 1MZR.
DR   InterPro; IPR001395; Aldo/ket_red.
DR   Pfam; PF00248; Aldo_ket_red; 1.
DR   PRINTS; PR00069; ALDKETRDTASE.
DR   ProDom; PD000288; Aldo/ket_red; 1.
DR   PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
SQ   SEQUENCE   330 AA;  35380 MW;  D746F858002EA448 CRC64;

  Query Match             50.5%;  Score 47;  DB 2;  Length 330;
  Best Local Similarity   50.0%;  Pred. No. 22;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IYPGDSDTRYSPSFQG 17
              ::| |    |||:|||
Db        220 VFPPDDWRAYSPTFQG 235


RESULT 14
O65840
ID   O65840      PRELIMINARY;      PRT;   155 AA.
AC   O65840;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   IAA amidohydrolase (Fragment).
OS   Linum usitatissimum (Flax) (Linseed).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Malpighiales; Linaceae; Linum.
OX   NCBI_TaxID=4006;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cotyledon;
RA   McKay G.J.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ005340; CAA06486.1; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF01546; Peptidase_M20; 1.
KW   Hydrolase.
FT   NON_TER       1      1
FT   NON_TER     155    155
SQ   SEQUENCE   155 AA;  17120 MW;  07B6DC3D472D31F1 CRC64;

  Query Match             49.5%;  Score 46;  DB 2;  Length 155;
  Best Local Similarity   61.5%;  Pred. No. 13;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GDSDTRYSPSFQG 17
              |:|:|: |||| |
Db         70 GESNTKVSPSFMG 82


RESULT 15
Q9ZB85
ID   Q9ZB85      PRELIMINARY;      PRT;   234 AA.
AC   Q9ZB85;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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```
DE   Protocatechuate 3,4-dioxygenase beta-subunit.
GN   Name=pcaH;
OS   Burkholderia gladioli.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=28095;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC10248;
RX   MEDLINE=97174572; PubMed=9022300;
RA   Petersen E., Zuegg J., Ribbons D.W., Schwab H.;
RT   "Molecular cloning and homology modeling of protocatechuate 3,4-
RT   dioxygenase from Pseudomonas marginata.";
RL   Microbiol. Res. 151:359-370(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC10248;
RA   Petersen E.I., Schwab H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U33634; AAC99961.1; -.
DR   HSSP; P00437; 3PCC.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0008199; F:ferric iron binding; IEA.
DR   GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
DR   GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR   InterPro; IPR000627; Dioxygenase.
DR   Pfam; PF00775; Dioxygenase_C; 1.
DR   PROSITE; PS00083; INTRADIOL_DIOXYGENAS; 1.
KW   Dioxygenase.
SQ   SEQUENCE   234 AA;  26534 MW;  1AA15AAF370D89AD CRC64;

  Query Match             49.5%;  Score 46;  DB 2;  Length 234;
  Best Local Similarity   53.3%;  Pred. No. 22;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 YPGDSDTRYSPSFQG 17
              :|||   :| |.|||
Db        178 FPGDPLLQYDPIFQG 192


Search completed: August 18, 2005, 06:18:13
Job time : 33.8975 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 15.1519 Seconds
(without alignments)
206.752 Million cell updates/sec

Title: US-10-684-957-36
Perfect score: 46
Sequence: 1 GSYFYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	100.0	8	17	US-10-684-957-36	Sequence 36, Appl
2	46	100.0	117	17	US-10-684-957-6	Sequence 6, Appli
3	46	100.0	447	17	US-10-684-957-17	Sequence 17, Appl
4	41	89.1	8	17	US-10-684-957-37	Sequence 37, Appl
5	41	89.1	117	17	US-10-684-957-10	Sequence 10, Appl
6	41	89.1	117	17	US-10-684-957-14	Sequence 14, Appl
7	41	89.1	117	17	US-10-684-957-30	Sequence 30, Appl
8	41	89.1	447	17	US-10-684-957-19	Sequence 19, Appl
9	41	89.1	447	17	US-10-684-957-21	Sequence 21, Appl
10	41	89.1	447	17	US-10-684-957-32	Sequence 32, Appl
11	39	84.8	120	17	US-10-938-353-104	Sequence 104, App
12	37	80.4	44	15	US-10-424-599-195094	Sequence 195094,
13	36	78.3	28	15	US-10-424-599-206372	Sequence 206372,
14	36	78.3	60	18	US-10-617-320-4381	Sequence 4381, Ap
15	36	78.3	95	16	US-10-437-963-127477	Sequence 127477,
16	36	78.3	313	16	US-10-767-701-44452	Sequence 44452, A
17	36	78.3	549	15	US-10-424-599-203330	Sequence 203330,
18	36	78.3	574	15	US-10-403-571-140	Sequence 140, App
19	36	78.3	599	16	US-10-425-115-268456	Sequence 268456,
20	36	78.3	631	15	US-10-425-114-42670	Sequence 42670, A
21	36	78.3	655	15	US-10-425-114-40391	Sequence 40391, A
22	36	78.3	680	15	US-10-425-114-46768	Sequence 46768, A
23	35	76.1	10	17	US-10-842-011-17	Sequence 17, Appl
24	35	76.1	10	17	US-10-842-011-32	Sequence 32, Appl
25	35	76.1	15	13	US-10-153-159-47	Sequence 47, Appl
26	35	76.1	15	14	US-10-153-176-47	Sequence 47, Appl
27	35	76.1	15	15	US-10-443-134A-47	Sequence 47, Appl
28	35	76.1	19	13	US-10-153-159-49	Sequence 49, Appl
29	35	76.1	19	13	US-10-153-159-50	Sequence 50, Appl
30	35	76.1	19	13	US-10-153-159-51	Sequence 51, Appl
31	35	76.1	19	13	US-10-153-159-54	Sequence 54, Appl
32	35	76.1	19	13	US-10-153-159-57	Sequence 57, Appl
33	35	76.1	19	13	US-10-153-159-58	Sequence 58, Appl
34	35	76.1	19	13	US-10-153-159-59	Sequence 59, Appl
35	35	76.1	19	14	US-10-153-176-49	Sequence 49, Appl
36	35	76.1	19	14	US-10-153-176-50	Sequence 50, Appl
37	35	76.1	19	14	US-10-153-176-51	Sequence 51, Appl
38	35	76.1	19	14	US-10-153-176-54	Sequence 54, Appl
39	35	76.1	19	14	US-10-153-176-57	Sequence 57, Appl
40	35	76.1	19	14	US-10-153-176-58	Sequence 58, Appl
41	35	76.1	19	14	US-10-153-176-59	Sequence 59, Appl
42	35	76.1	19	15	US-10-443-134A-49	Sequence 49, Appl
43	35	76.1	19	15	US-10-443-134A-50	Sequence 50, Appl
44	35	76.1	19	15	US-10-443-134A-51	Sequence 51, Appl
45	35	76.1	19	15	US-10-443-134A-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-10-684-957-36
; Sequence 36, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-36

Query Match 100.0%; Score 46; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 1 GSYFYFDL 8

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RESULT 2
US-10-684-957-6
; Sequence 6, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-6

  Query Match            100.0%;  Score 46;  DB 17;  Length 117;
  Best Local Similarity  100.0%;  Pred. No. 3.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              ||||||||
Db         99 GSYFYFDL 106


RESULT 3
US-10-684-957-17
; Sequence 17, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-684-957-17

  Query Match            100.0%;  Score 46;  DB 17;  Length 447;
  Best Local Similarity  100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              ||||||||
Db         99 GSYFYFDL 106


RESULT 4
US-10-684-957-37
; Sequence 37, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-37

  Query Match             89.1%;  Score 41;  DB 17;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db          1 GSYWYFDL 8


RESULT 5
US-10-684-957-10
; Sequence 10, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-10

  Query Match             89.1%;  Score 41;  DB 17;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 22;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106
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RESULT 6
US-10-684-957-14
; Sequence 14, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-14

  Query Match             89.1%;  Score 41;  DB 17;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 22;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106


RESULT 7
US-10-684-957-30
; Sequence 30, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-684-957-30

  Query Match             89.1%;  Score 41;  DB 17;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 22;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106


RESULT 8
US-10-684-957-19
; Sequence 19, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-19

  Query Match             89.1%;  Score 41;  DB 17;  Length 447;
  Best Local Similarity   87.5%;  Pred. No. 77;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106


RESULT 9
US-10-684-957-21
; Sequence 21, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-21

  Query Match             89.1%;  Score 41;  DB 17;  Length 447;
  Best Local Similarity   87.5%;  Pred. No. 77;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106


RESULT 10
US-10-684-957-32
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; Sequence 32, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-32

  Query Match             89.1%;  Score 41;  DB 17;  Length 447;
  Best Local Similarity   87.5%;  Pred. No. 77;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106


RESULT 11
US-10-938-353-104
; Sequence 104, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  DEVALARAJA, MADHAV NARASIMHA
;  APPLICANT:  FOLTZ, IAN
;  APPLICANT:  HAAK-FRENDSCHO, MARY
;  APPLICANT:  KELLERMANN, SIRID-AIMEE
;  APPLICANT:  LOW, JOSEPH EDWIN
;  APPLICANT:  MOBLEY, JAMES LESLIE
;  TITLE OF INVENTION: ANTIBODIES TO M-CSF
;  FILE REFERENCE: ABX-PF4
;  CURRENT APPLICATION NUMBER: US/10/938,353
;  CURRENT FILING DATE:  2004-09-09
;  PRIOR APPLICATION NUMBER: 60/502,163
;  PRIOR FILING DATE: 2003-09-10
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 104
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-353-104

  Query Match             84.8%;  Score 39;  DB 17;  Length 120;
  Best Local Similarity   85.7%;  Pred. No. 49;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              |||:|||
Db        101 GSYYYFD 107


RESULT 12
US-10-424-599-195094
; Sequence 195094, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195094
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_18197C.1.pep
US-10-424-599-195094

  Query Match             80.4%;  Score 37;  DB 15;  Length 44;
  Best Local Similarity   85.7%;  Pred. No. 41;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              :||||||
Db         36 NYFYFDL 42


RESULT 13
US-10-424-599-206372
; Sequence 206372, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206372
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_28380C.1.pep
US-10-424-599-206372

  Query Match             78.3%;  Score 36;  DB 15;  Length 28;
  Best Local Similarity   85.7%;  Pred. No. 39;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |||||
Db         15 GLYFYFD 21


RESULT 14
US-10-617-320-4381
; Sequence 4381, Application US/10617320
; Publication No. US20050136404A1
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                            SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNO
;                            THERAPEUTICS
;        NUMBER OF SEQUENCES: 5206
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
```

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;              CITY: Waltham
;              STATE: Massachusetts
;              COUNTRY: USA
;              ZIP: 02354
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: CD/ROM ISO9660
;              COMPUTER: <Unknown>
;              OPERATING SYSTEM: <Unknown>
;              SOFTWARE: <Unknown>
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/617,320
;              FILING DATE: 10-Jul-2003
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/107,433
;              FILING DATE: 30-Jun-1998
;              APPLICATION NUMBER: 60/ 085131
;              FILING DATE: May 12, 1998
;              APPLICATION NUMBER: 60/051553
;              FILING DATE: July 2, 1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Ariniello, Pamela Deneke
;              REGISTRATION NUMBER: 40,489
;              REFERENCE/DOCKET NUMBER: GTC-011
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (781)893-5007
;              TELEFAX: (781)893-8277
;    INFORMATION FOR SEQ ID NO: 4381:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 60 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         HYPOTHETICAL: YES
;         ORIGINAL SOURCE:
;              ORGANISM: Streptococcus pneumoniae
;         FEATURE:
;              NAME/KEY:  misc_feature
;              LOCATION: (B) LOCATION 1...60
;         SEQUENCE DESCRIPTION: SEQ ID NO: 4381:
US-10-617-320-4381

  Query Match            78.3%;  Score 36;  DB 18;  Length 60;
  Best Local Similarity  100.0%;  Pred. No. 80;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYF 6
              ||||||
Db          3 GSYFYF 8


RESULT 15
US-10-437-963-127477
; Sequence 127477, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 127477
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(95)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_29925C.1.pep
US-10-437-963-127477

  Query Match            78.3%;  Score 36;  DB 16;  Length 95;
  Best Local Similarity  85.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              |||||:|
Db         50 SYFYFEL 56


Search completed: August 18, 2005, 07:08:04
Job time : 16.2769 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 3.19435 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-36
Perfect score: 46
Sequence: 1 GSYFYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	84.8	114	2	S36280	Ig heavy chain V r
2	38	82.6	111	2	S26463	Ig heavy chain V r
3	38	82.6	122	2	B30515	Ig heavy chain V r
4	38	82.6	123	1	AVMS13	Ig heavy chain V r
5	36	78.3	90	2	A82562	hypothetical prote
6	36	78.3	146	2	G90337	hypothetical prote
7	36	78.3	190	2	F75336	conserved hypothet
8	36	78.3	216	2	C70649	hypothetical prote
9	36	78.3	405	2	AI3148	conserved hypothet
10	36	78.3	425	2	B98139	bme3 protein (AF07
11	36	78.3	547	2	T02910	pollen-specific pr
12	36	78.3	569	2	B70113	hypothetical prote
13	36	78.3	1144	2	A36968	P1-like adhesin pr
14	36	78.3	1508	2	T31098	probable dextransu
15	36	78.3	2817	2	B97033	uncharacterized pr
16	35	76.1	98	2	B24754	Ig heavy chain V r
17	35	76.1	112	2	S26327	Ig heavy chain V r
18	35	76.1	115	2	S13694	Ig heavy chain V r
19	35	76.1	116	2	S13691	Ig heavy chain V r
20	35	76.1	137	2	S03326	Ig heavy chain pre
21	35	76.1	294	2	G97915	choline-binding pr
22	35	76.1	332	2	T41227	hypothetical prote
23	35	76.1	332	2	H95043	choline binding pr
24	35	76.1	340	2	D95045	choline binding pr
25	35	76.1	594	2	F81359	para-aminobenzoate
26	34	73.9	91	2	S13689	Ig heavy chain V r
27	34	73.9	112	2	S18440	conserved hypothet
28	34	73.9	139	2	A41287	Ig heavy chain pre
29	34	73.9	278	2	S17710	kduI protein - Erw
30	34	73.9	278	2	AE0210	4-deoxy-L-threo-5-
31	34	73.9	302	2	T32317	hypothetical prote
32	34	73.9	564	2	AH2066	hypothetical prote
33	34	73.9	1365	2	A41483	glucosyltransferas
34	34	73.9	1449	2	T30857	glucosyltransferas
35	34	73.9	1449	2	T30552	glucosyltransferas
36	33	71.7	111	2	S13693	Ig heavy chain V r
37	33	71.7	154	2	PQ0465	beta C protein - P
38	33	71.7	168	2	B64032	hypothetical prote
39	33	71.7	194	1	XQEBHT	amidotransferase h
40	33	71.7	195	2	F81255	amidotransferase H
41	33	71.7	196	1	XQECHH	imidazole glycerol
42	33	71.7	196	2	AG0764	amidotransferase (
43	33	71.7	196	2	F85827	amidotransferase h
44	33	71.7	196	2	H90981	amidotransferase h
45	33	71.7	196	2	AE0188	amidotransferase (

ALIGNMENTS

RESULT 1
S36280
Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S36280
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36280
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-114 <GRI>
A;Cross-references: UNIPROT:Q9ULB6; EMBL:Z18822
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 39; DB 2; Length 114;
Best Local Similarity 85.7%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GSYFYFD 7
              |||:|||
Db        104 GSYYYFD 110
```

RESULT 2
S26463
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26463
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <KAV>
A;Cross-references: EMBL:X59113; NID:g51922; PIDN:CAA41839.1; PID:g51923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 38; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GSYFYFDL 8
              |||:|||:
```

```
Db         94 GSYWYFDV 101


RESULT 3
B30515
Ig heavy chain V region (5-1E4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 16-Aug-1996
C;Accession: B30515
R;Feeney, A.J.; Clarke, S.H.; Mosier, D.E.
J. Immunol. 141, 1267-1272, 1988
A;Title: Specific H chain junctional diversity may be required for non-T15 antibodies to
A;Reference number: A30515; MUID:88285740; PMID:3135325
A;Accession: B30515
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <FEE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 38;  DB 2;  Length 122;
  Best Local Similarity   75.0%;  Pred. No. 5.5;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:|||:
Db        104 GSYWYFDV 111


RESULT 4
AVMS13
Ig heavy chain V region (HPCG13) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: F93256
R;Gearhart, P.J.; Johnson, N.D.; Douglas, R.; Hood, L.
Nature 291, 29-34, 1981
A;Title: IgG antibodies to phosphorylcholine exhibit more diversity than their IgM count
A;Reference number: A93256; MUID:81197602; PMID:7231520
A;Accession: F93256
A;Molecule type: protein
A;Residues: 1-123 <GEA>
A;Cross-references: UNIPROT:P01793
A;Note: the possibility that some of the diversity seen in sequences of phosphorylcholin
C;Comment: This hybridoma protein binds phosphorylcholine.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

  Query Match             82.6%;  Score 38;  DB 1;  Length 123;
  Best Local Similarity   75.0%;  Pred. No. 5.6;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:|||:
Db        105 GSYWYFDV 112


RESULT 5
A82562
hypothetical protein XF2401 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82562
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82562
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <SIM>
A;Cross-references: UNIPROT:Q9PAU4; GB:AE004049; GB:AE003849; NID:g9107579; PIDN:AAF8520
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2401

  Query Match             78.3%;  Score 36;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 9.4;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFD 7
              ||||||
Db          5 SYFYFD 10


RESULT 6
G90337
hypothetical protein SSO1765 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90337
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-W
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <KUR>
A;Cross-references: UNIPROT:Q97XH6; GB:AE006641; NID:g13815008; PIDN:AAK41958.1; GSPDB:GN
C;Genetics:
A;Gene: SSO1765

  Query Match             78.3%;  Score 36;  DB 2;  Length 146;
  Best Local Similarity   75.0%;  Pred. No. 15;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              || ||||:
Db         29 GSMFYFDI 36


RESULT 7
F75336
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75336
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mak
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75336
A;Status: preliminary
```

A;Molecule type: DNA
A;Residues: 1-190 <WHI>
A;Cross-references: UNIPROT:Q9RT47; GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF1147
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1919
A;Map position: 1

Query Match 78.3%; Score 36; DB 2; Length 190;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
| :|||||
Db 114 GHWFYFDL 121

RESULT 8
C70649
hypothetical protein Rv3058c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: C70649
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70649
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-216 <COL>
A;Cross-references: UNIPROT:P95100; GB:Z83866; GB:AL123456; NID:g3261691; PIDN:CAB06264.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3058c

Query Match 78.3%; Score 36; DB 2; Length 216;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSYFYFD 7
| |||||
Db 57 GFYFYFD 63

RESULT 9
AI3148
conserved hypothetical protein bme3 [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3148
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3148
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <KUR>
A;Cross-references: UNIPROT:Q8U6J4; GB:AE008689; PIDN:AAL45607.1; PID:g17743327; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: bme3
A;Map position: linear chromosome

Query Match 78.3%; Score 36; DB 2; Length 405;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
|:|||| |
Db 88 GAYFYFKL 95

RESULT 10
B98139
bme3 protein (AF076290) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98139
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B98139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 <KUR>
A;Cross-references: UNIPROT:Q8U6J4; GB:AE007870; PIDN:AAK88636.1; PID:g15158357; GSPDB:G
C;Genetics:
A;Gene: AGR_L_143
A;Map position: linear chromosome

Query Match 78.3%; Score 36; DB 2; Length 425;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
|:|||| |
Db 108 GAYFYFKL 115

RESULT 11
T02910
pollen-specific protein homolog T13J8.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02910
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuel
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z14766
A;Accession: T02910
A;Molecule type: DNA
A;Residues: 1-547 <BEV>
A;Cross-references: UNIPROT:Q9SUD0; EMBL:AL035524
A;Experimental source: strain Columbia; BAC clone T13J8
C;Genetics:
A;Map position: 4
A;Introns: 47/3; 84/2; 174/3; 211/1; 449/2; 475/3
A;Note: T13J8.200
C;Superfamily: laccase

Query Match 78.3%; Score 36; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYF 6
||||||
Db 122 GSYFYF 127

RESULT 12
B70113
hypothetical protein BB0106 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: B70113
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70113
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-569 <KLE>
A;Cross-references: UNIPROT:O51133; GB:AE001123; GB:AE000783; NID:g2687987; PIDN:AAC6650
A;Experimental source: strain B31

  Query Match 78.3%; Score 36; DB 2; Length 569;
  Best Local Similarity 85.7%; Pred. No. 58;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSYFYFD 7
| |||||
Db 35 GFYFYFD 41

RESULT 13
A36968
P1-like adhesin precursor - Mycoplasma pirum
C;Species: Mycoplasma pirum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A36968
R;Tham, T.N.; Ferris, S.; Bahraoui, E.; Canarelli, S.; Montagnier, L.; Blanchard, A.
J. Bacteriol. 176, 781-788, 1994
A;Title: Molecular characterization of the P1-like adhesin gene from Mycoplasma pirum.
A;Reference number: A36968; MUID:94131957; PMID:8300531
A;Accession: A36968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1144 <THA>
A;Cross-references: UNIPROT:Q50371; GB:L19685; NID:g404770; PIDN:AAC36866.1; PID:g404771
C;Genetics:
A;Genetic code: SGC3

  Query Match 78.3%; Score 36; DB 2; Length 1144;
  Best Local Similarity 71.4%; Pred. No. 1.2e+02;
  Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFD 7
|:|:|||
Db 499 GTYYYFD 505

RESULT 14
T31098
probable dextransucrase (EC 2.4.1.5), extracellular - Leuconostoc mesenteroides
C;Species: Leuconostoc mesenteroides
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31098
R;Monchois, V.; Remaud-Simeon, M.; Monsan, P.; Willemot, R.M.
FEMS Microbiol. Lett. 159, 307-315, 1998
A;Title: Cloning and sequencing of a gene coding for an extracellular dextransucrase (DS
A;Reference number: Z20981; MUID:98164374; PMID:9503626
A;Accession: T31098
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1508 <MON>
A;Cross-references: UNIPROT:O52224; EMBL:AF030129; NID:g2766611; PID:g2766612; PIDN:AAB9
A;Experimental source: strain NRRL B-1299
C;Genetics:
A;Gene: dsrB
C;Function:
A;Description: produces dextran composed only of alpha(1-6) glucosidic bonds
C;Keywords: glycosyltransferase; hexosyltransferase

  Query Match 78.3%; Score 36; DB 2; Length 1508;
  Best Local Similarity 71.4%; Pred. No. 1.5e+02;
  Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFD 7
|:|:|||
Db 1172 GNYYYFD 1178

RESULT 15
B97033
uncharacterized protein, related to enterotoxins of other Clostridiales [imported] - Clos
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97033
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97033
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2817 <KUR>
A;Cross-references: UNIPROT:Q97K42; GB:AE001437; PIDN:AAK79053.1; PID:g15023993; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1079

  Query Match 78.3%; Score 36; DB 2; Length 2817;
  Best Local Similarity 71.4%; Pred. No. 2.9e+02;
  Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFD 7
|:|:|||
Db 525 GNYYYFD 531

Search completed: August 18, 2005, 06:20:10
Job time : 4.19435 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 15.0106 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-36
Perfect score: 46
Sequence: 1 GSYFYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	87.0	181	2	Q7VJ53	Q7vj53 helicobacte
2	38	82.6	123	1	HV24_MOUSE	P01793 mus musculu
3	38	82.6	470	2	Q7TMK1	Q7tmk1 mus musculu
4	37	80.4	297	2	Q6GP49	Q6gp49 xenopus lae
5	37	80.4	677	2	Q83FA6	Q83fa6 coxiella bu
6	36	78.3	90	2	Q87BM7	Q87bm7 xylella fas
7	36	78.3	90	2	Q9PAU4	Q9pau4 xylella fas
8	36	78.3	116	2	Q9UL89	Q9ul89 homo sapien
9	36	78.3	146	2	Q97XH6	Q97xh6 sulfolobus
10	36	78.3	190	2	Q9RT47	Q9rt47 deinococcus
11	36	78.3	194	1	HIS5_PYRFU	P58789 pyrococcus
12	36	78.3	210	1	HIS5_PHOPR	P62448 photobacter
13	36	78.3	210	2	Q65M42	Q65m42 bacillus li
14	36	78.3	216	2	P95100	P95100 mycobacteri
15	36	78.3	216	2	Q7TXC7	Q7txc7 mycobacteri
16	36	78.3	217	2	Q73VA6	Q73va6 mycobacteri
17	36	78.3	237	2	Q7D673	Q7d673 mycobacteri
18	36	78.3	268	2	Q7PYA6	Q7pya6 anopheles g
19	36	78.3	284	1	KDUI_XANAC	Q8pr01 xanthomonas
20	36	78.3	284	1	KDUI_XANCP	Q8pe32 xanthomonas
21	36	78.3	372	2	Q6G2F2	Q6g2f2 bartonella
22	36	78.3	385	2	Q9C0Y9	Q9c0y9 schizosacch
23	36	78.3	399	2	Q72R86	Q72r86 leptospira
24	36	78.3	399	2	Q8F4I9	Q8f4i9 leptospira
25	36	78.3	405	2	Q8RAL5	Q8ral5 thermoanaer
26	36	78.3	405	2	Q8U6J4	Q8u6j4 agrobacteri
27	36	78.3	425	2	Q7CVX9	Q7cvx9 agrobacteri
28	36	78.3	452	2	Q7QL63	Q7ql63 anopheles g
29	36	78.3	455	2	Q7PQF0	Q7pqf0 anopheles g
30	36	78.3	498	2	Q9LR17	Q9lr17 arabidopsis
31	36	78.3	545	2	Q8L8N6	Q8l8n6 arabidopsis
32	36	78.3	547	2	Q9SUD0	Q9sud0 arabidopsis
33	36	78.3	569	2	O51133	O51133 borrelia bu
34	36	78.3	661	2	Q973L1	Q97311 sulfolobus
35	36	78.3	681	2	Q8JHG9	Q8jhg9 brachydanio
36	36	78.3	794	2	Q7ZUK4	Q7zuk4 brachydanio
37	36	78.3	1111	2	Q63TC2	Q63tc2 burkholderi
38	36	78.3	1144	2	Q50371	Q50371 mycoplasma
39	36	78.3	1330	2	Q84CN4	Q84cn4 leuconostoc
40	36	78.3	1477	2	Q9L466	Q91466 leuconostoc
41	36	78.3	1508	2	O52224	O52224 leuconostoc
42	36	78.3	1508	2	Q9EZH5	Q9ezh5 leuconostoc
43	36	78.3	2817	2	Q97K42	Q97k42 clostridium
44	35	76.1	170	2	Q925S2	Q925s2 mus musculu
45	35	76.1	194	2	Q6LKJ6	Q6lkj6 photobacter

ALIGNMENTS

RESULT 1
Q7VJ53
ID Q7VJ53 PRELIMINARY; PRT; 181 AA.
AC Q7VJ53;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=HH0390;
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
DR EMBL; AE017145; AAP76987.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 181 AA; 21110 MW; 17B6E8ECA507755F CRC64;

Query Match 87.0%; Score 40; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 SYFYFDL 8
              |||||||
Db         20 SYFYFDL 26
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RESULT 2
HV24_MOUSE
ID HV24_MOUSE STANDARD; PRT; 123 AA.
AC P01793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V region HPCG13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than their

```
RT   IgM counterparts.";
RL   Nature 291:29-34(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC       binds phosphorylcholine.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; F93256; AVMS13.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1    114       Ig-like.
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  13808 MW;  6599F256ECCEDE50 CRC64;

  Query Match             82.6%;  Score 38;  DB 1;  Length 123;
  Best Local Similarity   75.0%;  Pred. No. 22;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:|||:
Db        105 GSYWYFDV 112


RESULT 3
Q7TMK1
ID   Q7TMK1      PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
DR   HSSP; P01865; 1KB5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match             82.6%;  Score 38;  DB 2;  Length 470;
  Best Local Similarity   75.0%;  Pred. No. 87;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:|||:
Db        122 GSYWYFDV 129


RESULT 4
Q6GP49
ID   Q6GP49      PRELIMINARY;      PRT;   297 AA.
AC   Q6GP49;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80677 protein.
GN   Name=MGC80677;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073295; AAH73295.1; -.
DR   GO; GO:0008146; F:sulfotransferase activity; IEA.
DR   InterPro; IPR000863; Sulfotransferase.
DR   Pfam; PF00685; Sulfotransfer_1; 1.
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DR   ProDom; PD001218; Sulfotransferase; 1.
SQ   SEQUENCE   297 AA;  34860 MW;  88D37337F60C6603 CRC64;

  Query Match             80.4%;  Score 37;  DB 2;  Length 297;
  Best Local Similarity   85.7%;  Pred. No. 83;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              ||:||||
Db        140 SYYYFDL 146


RESULT 5
Q83FA6
ID   Q83FA6      PRELIMINARY;      PRT;   677 AA.
AC   Q83FA6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Oligopeptidase A.
GN   Name=prlC; OrderedLocusNames=CBU0039;
OS   Coxiella burnetii.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Coxiellaceae; Coxiella.
OX   NCBI_TaxID=777;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nine Mile phase I / RSA 493;
RX   MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA   Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA   Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
RA   DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA   Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA   Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT   "Complete genome sequence of the Q-fever pathogen, Coxiella
RT   burnetii.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC   -!- COFACTOR: Binds 1 zinc ion (By similarity).
CC   -!- SIMILARITY: Belongs to peptidase family M3.
DR   EMBL; AE016960; AAO89608.1; -.
DR   TIGR; CBU0039; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001567; Pept_M3A_M3B.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01432; Peptidase_M3; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Complete proteome; Hydrolase; Metalloprotease; Zinc.
SQ   SEQUENCE   677 AA;  78213 MW;  68730738855A168F CRC64;

  Query Match             80.4%;  Score 37;  DB 2;  Length 677;
  Best Local Similarity   85.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              :||||||
Db        403 AYFYFDL 409


RESULT 6
Q87BM7
ID   Q87BM7      PRELIMINARY;      PRT;    90 AA.
AC   Q87BM7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=PD1421;
OS   Xylella fastidiosa (strain Temecula1 / ATCC 700964).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xylella.
OX   NCBI_TaxID=183190;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22421331; PubMed=12533478;
RX   DOI=10.1128/JB.185.3.1018-1026.2003;
RA   Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA   Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA   Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA   Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
RA   Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA   Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA   Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA   Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA   da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA   Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
RA   de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA   Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA   Kitajima J.P.;
RT   "Comparative analyses of the complete genome sequences of Pierce's
RT   disease and citrus variegated chlorosis strains of Xylella
RT   fastidiosa.";
RL   J. Bacteriol. 185:1018-1026(2003).
DR   EMBL; AE012558; AAO29268.1; -.
KW   Complete proteome.
SQ   SEQUENCE   90 AA;  9908 MW;  C69E7E2F76A174FD CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFD 7
              ||||||
Db          5 SYFYFD 10


RESULT 7
Q9PAU4
ID   Q9PAU4      PRELIMINARY;      PRT;    90 AA.
AC   Q9PAU4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=Xf2401;
OS   Xylella fastidiosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xylella.
OX   NCBI_TaxID=2371;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=9a5c;
RX   MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA   Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA   Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA   Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA   Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA   Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA   Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA   Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA   Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA   Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA   Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA   Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA   Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA   Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA   Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA   Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA   Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA   Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA   de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA   Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA   Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA   de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA   da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
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RA   da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA   de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA   Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA   Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT   "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL   Nature 406:151-159(2000).
DR   EMBL; AE004049; AAF85200.1; -.
DR   PIR; A82562; A82562.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   90 AA;  9720 MW;  5E2FD2193395B279 CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFD 7
              ||||||
Db          5 SYFYFD 10


RESULT 8
Q9UL89
ID   Q9UL89      PRELIMINARY;      PRT;   116 AA.
AC   Q9UL89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035025; AAD56261.1; -.
DR   PIR; PH0870; PH0870.
DR   PIR; PH1671; PH1671.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12605 MW;  C8F9131DE13EA898 CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 116;
  Best Local Similarity   75.0%;  Pred. No. 48;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              | |:||||
Db         98 GPYWYFDL 105


RESULT 9
Q97XH6
ID   Q97XH6      PRELIMINARY;      PRT;   146 AA.
AC   Q97XH6;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein SSO1765.
GN   OrderedLocusNames=SSO1765;
OS   Sulfolobus solfataricus.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=2287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35092 / DSM 1617 / P2;
RX   MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
RA   She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA   Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA   De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA   Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA   Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA   Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA   Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT   "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR   EMBL; AE006787; AAK41958.1; -.
DR   PIR; G90337; G90337.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   146 AA;  16953 MW;  77794A8649A99C21 CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 146;
  Best Local Similarity   75.0%;  Pred. No. 61;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              || ||||:
Db         29 GSMFYFDI 36


RESULT 10
Q9RT47
ID   Q9RT47      PRELIMINARY;      PRT;   190 AA.
AC   Q9RT47;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein DR1919.
GN   OrderedLocusNames=DR1919;
OS   Deinococcus radiodurans.
OC   Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX   MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
DR   EMBL; AE002031; AAF11472.1; -.
DR   PIR; F75336; F75336.
DR   TIGR; DR1919; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   190 AA;  21327 MW;  30326C4982CC4721 CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 190;
  Best Local Similarity   75.0%;  Pred. No. 80;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              | :|||||
Db        114 GHWFYFDL 121


RESULT 11
HIS5_PYRFU
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ID   HIS5_PYRFU     STANDARD;      PRT;   194 AA.
AC   P58789;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP
DE   synthase glutamine amidotransferase subunit) (IGP synthase subunit
DE   hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH).
GN   Name=hisH; OrderedLocusNames=PF1661;
OS   Pyrococcus furiosus.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=2261;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA   Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT   "The complete sequence of the Pyrococcus furiosus genome.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
CC       IGP, AICAR and glutamate. The hisH subunit provides the glutamine
CC       amidotransferase activity that produces the ammonia necessary to
CC       hisF for the synthesis of IGP and AICAR (By similarity).
CC   -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-
CC       ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC       carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
CC       aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC   -!- PATHWAY: Histidine biosynthesis; fifth step.
CC   -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE010265; AAL81785.1; -.
DR   HSSP; Q9X0C8; 1GPW.
DR   HAMAP; MF_00278; -; 1.
DR   InterPro; IPR000991; GATase_1.
DR   InterPro; IPR010139; IMP_synth_hisH.
DR   Pfam; PF00117; GATase; 1.
DR   PRINTS; PR00096; GATASE.
DR   TIGRFAMs; TIGR01855; IMP_synth_hisH; 1.
DR   PROSITE; PS00442; GATASE_TYPE_I; 1.
KW   Complete proteome; Glutamine amidotransferase; Histidine biosynthesis;
KW   Transferase.
FT   ACT_SITE     74     74       By similarity.
FT   ACT_SITE    176    176       By similarity.
FT   ACT_SITE    178    178       By similarity.
SQ   SEQUENCE   194 AA;  21660 MW;  106E39F9DFC6FED9 CRC64;

  Query Match             78.3%;  Score 36;  DB 1;  Length 194;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYF 6
              ||||||
Db        131 GSYFYF 136


RESULT 12
HIS5_PHOPR
ID   HIS5_PHOPR     STANDARD;      PRT;   210 AA.
AC   P62448;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP
DE   synthase glutamine amidotransferase subunit) (IGP synthase subunit
DE   hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH).
GN   Name=hisH; OrderedLocusNames=PBPRA1088;
OS   Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Photobacterium.
OX   NCBI_TaxID=74109;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA   Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA   Valle G.;
RT   "Genome analysis of Photobacterium profundum reveals the complexity of
RT   high pressure adaptations.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
CC       IGP, AICAR and glutamate. The hisH subunit provides the glutamine
CC       amidotransferase activity that produces the ammonia necessary to
CC       hisF for the synthesis of IGP and AICAR (By similarity).
CC   -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-
CC       ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC       carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
CC       aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC   -!- PATHWAY: Histidine biosynthesis; fifth step.
CC   -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; CR378666; CAG19499.1; -.
DR   HAMAP; MF_00278; -; 1.
DR   PROSITE; PS00442; GATASE_TYPE_I; 1.
KW   Complete proteome; Glutamine amidotransferase; Histidine biosynthesis;
KW   Transferase.
FT   ACT_SITE     82     82       By similarity.
FT   ACT_SITE    192    192       By similarity.
FT   ACT_SITE    194    194       By similarity.
SQ   SEQUENCE   210 AA;  22896 MW;  FE525895F7985E15 CRC64;

  Query Match             78.3%;  Score 36;  DB 1;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYF 6
              ||||||
Db        146 GSYFYF 151


RESULT 13
Q65M42
ID   Q65M42      PRELIMINARY;      PRT;   210 AA.
AC   Q65M42;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   YhbJ (Single hybrid motif).
GN   Name=yhbJ; ORFNames=BL03188, BLi00964;
OS   Bacillus licheniformis DSM 13.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=279010;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 13;
RX   PubMed=15383718;
RA   Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA   Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
```

```
RA   Ehrenreich A., Gottschalk G.;
RT   "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT   Organism with Great Industrial Potential.";
RL   J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 14580;
RA   Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA   Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA   Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA   Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA   Berka R.M.;
RT   "Complete genome sequence of the industrial bacterium Bacillus
RT   licheniformis and comparisons with closely related Bacillus species.";
RL   Genome Biol. 5:R77-R77(2004).
DR   EMBL; AE017333; AAU39872.1; -.
DR   EMBL; CP000002; AAU22528.1; -.
SQ   SEQUENCE   210 AA;  22522 MW;  14A8ADE08D31E8A6 CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 210;
  Best Local Similarity   71.4%;  Pred. No. 89;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              |:|||:|
Db         24 GAYFYYD 30


RESULT 14
P95100
ID   P95100      PRELIMINARY;      PRT;   216 AA.
AC   P95100;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY TETR-
DE   FAMILY).
GN   OrderedLocusNames=Rv3058c;
OS   Mycobacterium tuberculosis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37Rv;
RX   MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA   Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA   Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA   Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA   Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA   Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA   Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT   "Deciphering the biology of Mycobacterium tuberculosis from the
RT   complete genome sequence.";
RL   Nature 393:537-544(1998).
CC   -!- SIMILARITY: Contains 1 HTH tetR-type DNA-binding domain.
DR   EMBL; BX842581; CAB06264.1; -.
DR   PIR; C70649; C70649.
DR   TubercuList; Rv3058c; -.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR009057; Homeodomain_like.
DR   InterPro; IPR001647; HTH_TetR.
DR   Pfam; PF00440; TetR_N; 1.
DR   PRINTS; PR00455; HTHTETR.
KW   Complete proteome; DNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   216 AA;  23835 MW;  BDD332678E39485F CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 216;
  Best Local Similarity   85.7%;  Pred. No. 92;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |||||
Db         57 GFYFYFD 63


RESULT 15
Q7TXC7
ID   Q7TXC7      PRELIMINARY;      PRT;   216 AA.
AC   Q7TXC7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY TETR-
DE   FAMILY).
GN   OrderedLocusNames=Mb3084c;
OS   Mycobacterium bovis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1765;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AF2122/97;
RX   MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA   Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA   Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA   Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA   Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT   "The complete genome sequence of Mycobacterium bovis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR   EMBL; BX248344; CAD96771.1; -.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR009057; Homeodomain_like.
DR   InterPro; IPR001647; HTH_TetR.
DR   Pfam; PF00440; TetR_N; 1.
KW   Complete proteome.
SQ   SEQUENCE   216 AA;  23835 MW;  BDD332678E39485F CRC64;

  Query Match             78.3%;  Score 36;  DB 2;  Length 216;
  Best Local Similarity   85.7%;  Pred. No. 92;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |||||
Db         57 GFYFYFD 63


Search completed: August 18, 2005, 06:18:16
Job time : 18.0106 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 17.2438 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-36
Perfect score: 46
Sequence: 1 GSYFYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	100.0	8	8	ADS87943	Ads87943 Anti-IFN-
2	46	100.0	8	8	ADS94940	Ads94940 Anti-IFN-
3	46	100.0	117	8	ADS87913	Ads87913 Anti-IFN-
4	46	100.0	117	8	ADS94910	Ads94910 Anti-IFN-
5	46	100.0	447	8	ADS87924	Ads87924 Anti-IFN-
6	46	100.0	447	8	ADS94921	Ads94921 Anti-IFN-
7	41	89.1	8	8	ADS87944	Ads87944 Anti-IFN-
8	41	89.1	8	8	ADS94941	Ads94941 Anti-IFN-
9	41	89.1	117	8	ADS87917	Ads87917 Anti-IFN-
10	41	89.1	117	8	ADS87921	Ads87921 Anti-IFN-
11	41	89.1	117	8	ADS87937	Ads87937 Anti-IFN-
12	41	89.1	117	8	ADS94914	Ads94914 Anti-IFN-
13	41	89.1	117	8	ADS94934	Ads94934 Anti-IFN-
14	41	89.1	117	8	ADS94918	Ads94918 Anti-IFN-
15	41	89.1	447	8	ADS87928	Ads87928 Anti-IFN-
16	41	89.1	447	8	ADS87926	Ads87926 Anti-IFN-
17	41	89.1	447	8	ADS87939	Ads87939 Anti-IFN-
18	41	89.1	447	8	ADS94936	Ads94936 Anti-IFN-
19	41	89.1	447	8	ADS94923	Ads94923 Anti-IFN-
20	41	89.1	447	8	ADS94925	Ads94925 Anti-IFN-
21	39	84.8	97	7	ADI40541	Adi40541 Human pur
22	37	80.4	191	3	AAG23810	Aag23810 Arabidops
23	37	80.4	250	3	AAG23809	Aag23809 Arabidops
24	36	78.3	60	8	ADR95746	Adr95746 Novel S.
25	36	78.3	117	2	AAW00831	Aaw00831 Variable
26	36	78.3	117	2	AAW19017	Aaw19017 Anti-huma
27	36	78.3	236	3	AAG23252	Aag23252 Arabidops
28	36	78.3	545	5	ABB91611	Abb91611 Herbicida
29	36	78.3	547	5	ABB93129	Abb93129 Herbicida
30	36	78.3	574	8	ADO57373	Ado57373 Kidney de
31	36	78.3	1144	2	AAR76059	Aar76059 Mycoplasm
32	35	76.1	10	7	ADD69225	Add69225 Human hea
33	35	76.1	10	7	ADD69228	Add69228 Human hea
34	35	76.1	15	8	ADG31813	Adg31813 Experimen
35	35	76.1	19	8	ADG31815	Adg31815 Anti-VEGF
36	35	76.1	19	8	ADG31817	Adg31817 Anti-VEGF
37	35	76.1	19	8	ADG31825	Adg31825 Variant p
38	35	76.1	19	8	ADG31820	Adg31820 Anti-VEGF
39	35	76.1	19	8	ADG31816	Adg31816 Anti-VEGF
40	35	76.1	19	8	ADG31823	Adg31823 Anti-VEGF
41	35	76.1	19	8	ADG31824	Adg31824 Anti-VEGF
42	35	76.1	20	5	ABP47138	Abp47138 Human BLy
43	35	76.1	20	6	ABR54853	Abr54853 Human imm
44	35	76.1	20	7	ADG97965	Adg97965 scFV VHCD
45	35	76.1	26	8	ADG31857	Adg31857 Anti-VEGF

ALIGNMENTS

RESULT 1
ADS87943
ID ADS87943 standard; peptide; 8 AA.
XX
AC ADS87943;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR3 SEQ ID NO:36.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87952.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 1; SEQ ID NO 36; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising

CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 46; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 1 GSYFYFDL 8

RESULT 2
ADS94940
ID ADS94940 standard; peptide; 8 AA.
XX
AC ADS94940;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR3 SEQ ID NO:36.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94949.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 1; SEQ ID NO 36; 115pp; English.

XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 46; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 1 GSYFYFDL 8

RESULT 3
ADS87913
ID ADS87913 standard; protein; 117 AA.
XX
AC ADS87913;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:6.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87912.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or

PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 6; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 99 GSYFYFDL 106

RESULT 4
ADS94910
ID ADS94910 standard; protein; 117 AA.
XX
AC ADS94910;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:6.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94909.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 6; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 46; DB 8; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 99 GSYFYFDL 106

RESULT 5
ADS87924
ID ADS87924 standard; protein; 447 AA.
XX
AC ADS87924;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;

XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 17; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 46; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 99 GSYFYFDL 106

RESULT 6
ADS94921
ID ADS94921 standard; protein; 447 AA.
XX
AC ADS94921;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 heavy chain SEQ ID NO:17.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 14; SEQ ID NO 17; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 46; DB 8; Length 447;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||||||
Db 99 GSYFYFDL 106

RESULT 7
ADS87944
ID ADS87944 standard; peptide; 8 AA.
XX
AC ADS87944;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR3 SEQ ID NO:37.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.

PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87953.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 1; SEQ ID NO 37; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 8 AA;

```
  Query Match             89.1%;  Score 41;  DB 8;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db          1 GSYWYFDL 8
```

RESULT 8
ADS94941
ID ADS94941 standard; peptide; 8 AA.
XX
AC ADS94941;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain CDR3 SEQ ID NO:37.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94950.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 1; SEQ ID NO 37; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 8 AA;

```
  Query Match             89.1%;  Score 41;  DB 8;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db          1 GSYWYFDL 8
```

RESULT 9
ADS87917
ID ADS87917 standard; protein; 117 AA.
XX
AC ADS87917;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:10.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX

PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87916.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 10; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

```
  Query Match             89.1%;  Score 41;  DB 8;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106
```

RESULT 10
ADS87921
ID ADS87921 standard; protein; 117 AA.
XX
AC ADS87921;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:14.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87920.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

```
  Query Match             89.1%;  Score 41;  DB 8;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 14;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106
```

RESULT 11
ADS87937
ID ADS87937 standard; protein; 117 AA.
XX
AC ADS87937;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:30.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;

KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87963.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 6; SEQ ID NO 30; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 89.1%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||:||||
Db 99 GSYWYFDL 106

RESULT 12
ADS94914
ID ADS94914 standard; protein; 117 AA.
XX
AC ADS94914;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:10.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94913.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 10; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 89.1%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||:||||
Db 99 GSYWYFDL 106

RESULT 13
ADS94934
ID ADS94934 standard; protein; 117 AA.
XX
AC ADS94934;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:30.

XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94960.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 30; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 89.1%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||:||||
Db 99 GSYWYFDL 106

RESULT 14
ADS94918
ID ADS94918 standard; protein; 117 AA.
XX
AC ADS94918;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody heavy chain variable region SEQ ID NO:14.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94917.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 8; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 117 AA;

Query Match 89.1%; Score 41; DB 8; Length 117;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSYFYFDL 8
||||:||||
Db 99 GSYWYFDL 106

RESULT 15

ADS87928
ID ADS87928 standard; protein; 447 AA.
XX
AC ADS87928;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 or 1121* heavy chain SEQ ID NO:21.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 12; SEQ ID NO 21; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma heavy chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 447 AA;

Query Match 89.1%; Score 41; DB 8; Length 447;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GSYFYFDL 8
              |||:||||
Db         99 GSYWYFDL 106
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Search completed: August 18, 2005, 06:09:15
Job time : 18.2438 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 6.74205 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-38
Perfect score: 53
Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	100.0	12	4	US-09-563-222C-11	Sequence 11, Appl
2	53	100.0	96	4	US-09-472-087-87	Sequence 87, Appl
3	53	100.0	107	2	US-08-652-558-49	Sequence 49, Appl
4	53	100.0	108	1	US-08-488-113B-150	Sequence 150, App
5	53	100.0	108	1	US-08-477-484B-150	Sequence 150, App
6	53	100.0	108	2	US-08-646-360-150	Sequence 150, App
7	53	100.0	108	2	US-08-232-081B-42	Sequence 42, Appl
8	53	100.0	108	3	US-08-839-765-150	Sequence 150, App
9	53	100.0	108	3	US-09-136-389-150	Sequence 150, App
10	53	100.0	108	3	US-09-610-838-150	Sequence 150, App
11	53	100.0	108	4	US-09-711-485-150	Sequence 150, App
12	53	100.0	109	3	US-09-025-769B-16	Sequence 16, Appl
13	53	100.0	109	4	US-09-490-070A-16	Sequence 16, Appl
14	53	100.0	109	4	US-09-490-153-16	Sequence 16, Appl
15	53	100.0	109	4	US-09-490-324-16	Sequence 16, Appl
16	53	100.0	110	3	US-09-025-769B-30	Sequence 30, Appl
17	53	100.0	110	3	US-09-025-769B-47	Sequence 47, Appl
18	53	100.0	110	4	US-09-490-070A-30	Sequence 30, Appl
19	53	100.0	110	4	US-09-490-070A-47	Sequence 47, Appl
20	53	100.0	110	4	US-09-490-153-30	Sequence 30, Appl
21	53	100.0	110	4	US-09-490-153-47	Sequence 47, Appl
22	53	100.0	110	4	US-09-490-324-30	Sequence 30, Appl
23	53	100.0	110	4	US-09-490-324-47	Sequence 47, Appl
24	53	100.0	116	1	US-08-053-131-183	Sequence 183, App
25	53	100.0	116	2	US-08-096-762-183	Sequence 183, App
26	53	100.0	116	3	US-09-042-353-46	Sequence 46, Appl
27	53	100.0	116	3	US-08-758-417A-311	Sequence 311, App
28	53	100.0	150	3	US-08-862-124-5	Sequence 5, Appli
29	53	100.0	224	4	US-09-456-090A-40	Sequence 40, Appl
30	53	100.0	224	4	US-09-456-090A-52	Sequence 52, Appl
31	53	100.0	224	4	US-09-456-090A-76	Sequence 76, Appl
32	53	100.0	224	4	US-09-453-234-40	Sequence 40, Appl
33	53	100.0	224	4	US-09-453-234-52	Sequence 52, Appl
34	53	100.0	224	4	US-09-453-234-76	Sequence 76, Appl
35	53	100.0	226	4	US-09-456-090A-38	Sequence 38, Appl
36	53	100.0	226	4	US-09-456-090A-42	Sequence 42, Appl
37	53	100.0	226	4	US-09-456-090A-50	Sequence 50, Appl
38	53	100.0	226	4	US-09-456-090A-80	Sequence 80, Appl
39	53	100.0	226	4	US-09-456-090A-86	Sequence 86, Appl
40	53	100.0	226	4	US-09-453-234-38	Sequence 38, Appl
41	53	100.0	226	4	US-09-453-234-42	Sequence 42, Appl
42	53	100.0	226	4	US-09-453-234-50	Sequence 50, Appl
43	53	100.0	226	4	US-09-453-234-80	Sequence 80, Appl
44	53	100.0	226	4	US-09-453-234-86	Sequence 86, Appl
45	53	100.0	287	3	US-08-862-124-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-563-222C-11
; Sequence 11, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-11

Query Match 100.0%; Score 53; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 2
US-09-472-087-87
; Sequence 87, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647

```
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-87

  Query Match            100.0%;  Score 53;  DB 4;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 0.009;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 3
US-08-652-558-49
; Sequence 49, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-49

  Query Match            100.0%;  Score 53;  DB 2;  Length 107;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 4
US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-150

  Query Match            100.0%;  Score 53;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 5
US-08-477-484B-150
; Sequence 150, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
```

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;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-150

  Query Match             100.0%;  Score 53;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 6
US-08-646-360-150
; Sequence 150, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-150

  Query Match             100.0%;  Score 53;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 7
US-08-232-081B-42
; Sequence 42, Application US/08232081B
; Patent No. 5886152
;  GENERAL INFORMATION:
;    APPLICANT:  NAKATANI, TOMOYUKI
;    APPLICANT:  GOMI, HIDEYUKI
;    APPLICANT:  WIJDENES, JOHN
;    APPLICANT:  NOGUCHI, HIROSHI
;    TITLE OF INVENTION:  HUMANIZED B-B10
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
```

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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,081B
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SVENSSON, LEONARD R
;       REGISTRATION NUMBER:  30,330
;       REFERENCE/DOCKET NUMBER:  20-3484
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 205-8000
;       TELEFAX:  (703) 205-8050
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  108 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-232-081B-42

  Query Match             100.0%;  Score 53;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 8
US-08-839-765-150
; Sequence 150, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-150

  Query Match             100.0%;  Score 53;  DB 3;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 9
US-09-136-389-150
; Sequence 150, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
```

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-150

  Query Match           100.0%;  Score 53;  DB 3;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 10
US-09-610-838-150
; Sequence 150, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/610,838
;      FILING DATE:  06-JUL-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:  18-AUG-1998
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-610-838-150

  Query Match           100.0%;  Score 53;  DB 3;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 11
US-09-711-485-150
; Sequence 150, Application US/09711485
; Patent No. 6649742
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/711,485
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,765
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
```

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;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  150:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  108 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-711-485-150

  Query Match             100.0%;  Score 53;  DB 4;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 12
US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;     APPLICANT:  Knappik, Achim
;     APPLICANT:  Pack, Peter
;     APPLICANT:  Ilag, Vic
;     APPLICANT:  Ge, Liming
;     APPLICANT:  Moroney, Simon
;     APPLICANT:  Plueckthun, Andreas
;     TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;     NUMBER OF SEQUENCES:  373
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;       STREET:  1251 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10021
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/025,769B
;       FILING DATE:  18-FEB-1998
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP 95 11 3021.0
;       FILING DATE:  18-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  James F. Haley, Jr., Esq.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  MORPHO/5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)596-9000
;       TELEFAX:  (212)596-9090
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  109 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-025-769B-16

  Query Match             100.0%;  Score 53;  DB 3;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 13
US-09-490-070A-16
; Sequence 16, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                       White & McAuliffe
;            STREET: 1666 K Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,070A
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Colin G. Sandercock, Esq.
;            REGISTRATION NUMBER: 31,298
;            REFERENCE/DOCKET NUMBER: 37629-0005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 912-2000
;            TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 16:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 109 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-070A-16

  Query Match             100.0%;  Score 53;  DB 4;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 14
US-09-490-153-16
; Sequence 16, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
```

```
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10021
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,153
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/025,769B
;             FILING DATE: 18-FEB-1998
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: James F. Haley, Jr., Esq.
;             REGISTRATION NUMBER: 27,794
;             REFERENCE/DOCKET NUMBER: MORPHO/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)596-9000
;             TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 109 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-153-16

  Query Match           100.0%;  Score 53;  DB 4;  Length 109;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 15
US-09-490-324-16
; Sequence 16, Application US/09490324
; Patent No. 6828422
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10021
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,324
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/025,769
;             FILING DATE: 18-FEB-1998
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: James F. Haley, Jr., Esq.
;             REGISTRATION NUMBER: 27,794
;             REFERENCE/DOCKET NUMBER: MORPHO/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)596-9000
;             TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 109 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-324-16

  Query Match           100.0%;  Score 53;  DB 4;  Length 109;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 25.8657 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-38
Perfect score: 53
Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	100.0	12	2	AAR15375	Aar15375 IgM-RF Gl
2	53	100.0	12	5	AAU70331	Aau70331 Human Kap
3	53	100.0	12	5	AAU83718	Aau83718 MS-GPC-6
4	53	100.0	12	5	ABB57480	Abb57480 HLA-DR-sp
5	53	100.0	12	5	ABB57475	Abb57475 HLA-DR-sp
6	53	100.0	12	5	ABB57469	Abb57469 HLA-DR-sp
7	53	100.0	12	5	ABB57472	Abb57472 HLA-DR-sp
8	53	100.0	12	6	AAE38096	Aae38096 Human COU
9	53	100.0	12	6	AAE38067	Aae38067 Human 17G
10	53	100.0	12	6	ADA90302	Ada90302 MS-Roche
11	53	100.0	12	6	ADA90308	Ada90308 MS-Roche
12	53	100.0	12	6	ADA90317	Ada90317 MS-Roche
13	53	100.0	12	6	ADA90323	Ada90323 MS-Roche
14	53	100.0	12	6	ADA90324	Ada90324 MS-Roche
15	53	100.0	12	6	ADA90641	Ada90641 MS-Roche
16	53	100.0	12	6	ADA90751	Ada90751 MS-Roche
17	53	100.0	12	6	ADA90867	Ada90867 MS-Roche
18	53	100.0	12	6	ADA90869	Ada90869 MS-Roche
19	53	100.0	12	6	ADA91097	Ada91097 MS-R Fab/
20	53	100.0	12	6	ADA90322	Ada90322 MS-Roche
21	53	100.0	12	6	ADA90487	Ada90487 MS-Roche
22	53	100.0	12	6	ADA90497	Ada90497 MS-Roche
23	53	100.0	12	6	ADA90871	Ada90871 MS-Roche
24	53	100.0	12	6	ADA90953	Ada90953 MS-R Fab/
25	53	100.0	12	6	ADA91010	Ada91010 MS-R Fab/
26	53	100.0	12	6	ADA91235	Ada91235 MS-R Fab/
27	53	100.0	12	6	ADA91241	Ada91241 MS-R Fab/
28	53	100.0	12	6	ADA90301	Ada90301 MS-Roche
29	53	100.0	12	6	ADA90309	Ada90309 MS-Roche
30	53	100.0	12	6	ADA90488	Ada90488 MS-Roche
31	53	100.0	12	6	ADA90637	Ada90637 MS-Roche
32	53	100.0	12	6	ADA90756	Ada90756 MS-Roche
33	53	100.0	12	6	ADA90313	Ada90313 MS-Roche
34	53	100.0	12	6	ADA90320	Ada90320 MS-Roche
35	53	100.0	12	6	ADA90484	Ada90484 MS-Roche
36	53	100.0	12	6	ADA90490	Ada90490 MS-Roche
37	53	100.0	12	6	ADA90631	Ada90631 MS-Roche
38	53	100.0	12	6	ADA90643	Ada90643 MS-Roche
39	53	100.0	12	6	ADA90989	Ada90989 MS-R Fab/
40	53	100.0	12	6	ADA91339	Ada91339 MS-R Fab/
41	53	100.0	12	6	ADA90315	Ada90315 MS-Roche
42	53	100.0	12	6	ADA90321	Ada90321 MS-Roche
43	53	100.0	12	6	ADA90325	Ada90325 MS-Roche
44	53	100.0	12	6	ADA90479	Ada90479 MS-Roche
45	53	100.0	12	6	ADA90495	Ada90495 MS-Roche

ALIGNMENTS

RESULT 1
AAR15375
ID AAR15375 standard; protein; 12 AA.
XX
AC AAR15375;
XX
DT 25-MAR-2003 (revised)
DT 05-MAR-1992 (first entry)
XX
DE IgM-RF Glo.
XX
KW Rheumatoid factor; RF; antigen; CDR; IgM.
XX
OS Synthetic.
XX
PN US5068177-A.
XX
PD 26-NOV-1991.
XX
PF 05-AUG-1985; 85US-00762698.
XX
PR 05-AUG-1985; 85US-00762698.
XX
PA (SCRI) SCRIPPS CLINIC & RES FOUND.
XX
PI Carson DA, Fong S, Chen PP;
XX
DR WPI; 1991-368612/50.
XX
PT Synthetic polypeptide(s) for inducing anti-idiotype antibodies - useful
PT for treating auto immune-, endocrine- and rheumatic-diseases and
PT myasthenia gravis.
XX
PS Claim 10; Page 42; 44pp; English.
XX
CC Three rabbits were inoculated with two s.c. injections of PGL1 (synthetic
CC peptide) conjugated to KLH as an immunogen, and their sera were analysed
CC for anti-peptide antibody activity by ELISA. All three immunised rabbits
CC produced anti-PGL1 antibody. Antisera drawn from a rabbit on two
CC different days reacted significantly with the corresp. intact IgM-RF Glo.
CC See also AAR15365-74 and AAR15375. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          1 RASQSVSSSYLA 12
```

RESULT 2
AAU70331
ID AAU70331 standard; peptide; 12 AA.
XX
AC AAU70331;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Kappa III light chain CDR1.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Page 14; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 12 AA;

```
  Query Match             100.0%;  Score 53;  DB 5;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          1 RASQSVSSSYLA 12
```

RESULT 3
AAU83718
ID AAU83718 standard; peptide; 12 AA.
XX
AC AAU83718;
XX
DT 08-MAY-2002 (first entry)
XX
DE MS-GPC-6 light chain variable region CD1 sequence.
XX
KW Human; antibody-based antigen; HLA-DR; CDR; antibody;
KW human leukocyte antigen; cell proliferative disorder; lymphoma;
KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
KW Grave's disease; insulin-dependent diabetes; transplant rejection;
KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
KW IL-2; MS-GPC; complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200187337-A1.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015625.
XX
PR 12-MAY-2000; 2000EP-00110065.
PR 06-OCT-2000; 2000US-0238492P.
XX
PA (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
PI Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
XX
DR WPI; 2002-075288/10.
XX
PT Polypeptide compositions which bind to cell surface epitopes, which in
PT multivalent form kills lymphoid tumor cells and in monovalent form causes
PT immunosuppression or inhibits activation of lymphocytes.
XX
PS Example 4; Page 66; 150pp; English.
XX
CC The invention relates to a composition which includes a polypeptide or a
CC multivalent polypeptide comprising one or more antibody-based antigen -
CC binding domain of human composition with binding specificity for an
CC antigen expressed on surface of a human cell, especially HLA-DR (human
CC leukocyte antigen DR), where treating cells expressing HLA-DR with the
CC multivalent polypeptide causes or leads to killing of cells without need
CC of cytotoxic entities or immunological mechanisms. Also included are the
CC nucleic acid encoding the polypeptide, a vector comprising the nucleic
CC acid and a host cell harbouring vector or nucleic acid. The polypeptide
CC (optionally linked to cytotoxic or immunogenic agent), the nucleic acid
CC and the host cell are useful for preparing a pharmaceutical preparation
CC for the treatment of cell proliferative disorders, disorders involving
CC transformed cells expressing MHC class II antigens, B cell non-Hodgkin's
CC lymphoma, B cell lymphoma, B cell acute lymphoid leukemia, Burkitt's
CC lymphoma, Hodgkin's lymphoma, hairy cell leukaemia, acute myeloid
CC leukaemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic
CC myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid
CC leukaemia, disorders involving unwanted activation of the cells of the
CC immune system, such as lymphoid cells expressing MHC class II, rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's diseases,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft vs.
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The
CC antigen is useful for suppressing activation or proliferation of a cell
CC of the immune system, suppressing interleukin-2 (IL-2) secretion by a
CC cell of the immune system, such as expressing HLA-DR, the interaction of
CC the cell of the immune system with another cell, immunosuppressing a
CC patient and for killing a cell expressing an antigen, HLA-DR on the
CC surface of the cell, where neither cytotoxic entities nor immunological

CC mechanisms are needed to cause or lead to the killing. The killing is
CC dependent on the action of non-caspase proteases and/or cannot be
CC inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a
CC complementarity determining region (CDR) based on the human antigen
CC binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are
CC either the native sequence or have been optimised/mutated to alter their
CC antigen binding capabilities
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 4
ABB57480
ID ABB57480 standard; peptide; 12 AA.
XX
AC ABB57480;
XX
DT 18-MAR-2002 (first entry)
XX
DE HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-6.
XX
KW Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antirheumatic; antiarthritic;
KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;
KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200187338-A1.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015626.
XX
PR 12-MAY-2000; 2000EP-00110063.
PR 06-OCT-2000; 2000US-0238762P.
XX
PA (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
PI Nagy Z, Tesar M, Thomassen-Wolf E;
XX
DR WPI; 2002-075289/10.
XX
PT Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
PS Example; Page 60; 139pp; English.
XX
CC The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 5
ABB57475
ID ABB57475 standard; peptide; 12 AA.
XX
AC ABB57475;
XX
DT 18-MAR-2002 (first entry)
XX
DE HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-4.
XX
KW Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antirheumatic; antiarthritic;
KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;
KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200187338-A1.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015626.
XX
PR 12-MAY-2000; 2000EP-00110063.
PR 06-OCT-2000; 2000US-0238762P.
XX
PA (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
PI Nagy Z, Tesar M, Thomassen-Wolf E;
XX
DR WPI; 2002-075289/10.

XX
PT Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
PS Example; Page 60; 139pp; English.
XX
CC The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 6
ABB57469
ID ABB57469 standard; peptide; 12 AA.
XX
AC ABB57469;
XX
DT 18-MAR-2002 (first entry)
XX
DE HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-2.
XX
KW Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antirheumatic; antiarthritic;
KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;
KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200187338-A1.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015626.
XX
PR 12-MAY-2000; 2000EP-00110063.
PR 06-OCT-2000; 2000US-0238762P.
XX
PA (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
PI Nagy Z, Tesar M, Thomassen-Wolf E;
XX
DR WPI; 2002-075289/10.
XX
PT Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
PS Example; Page 60; 139pp; English.
XX
CC The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 7
ABB57472
ID ABB57472 standard; peptide; 12 AA.
XX
AC ABB57472;
XX
DT 18-MAR-2002 (first entry)
XX
DE HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-3.
XX
KW Immunomodulatory human MHC class II antigen-binding protein; HLA;
KW human leukocyte antigen; immune system; immunosuppression; antibody;
KW major histocompatibility complex; antirheumatic; antiarthritic;
KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;

```
KW   thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
KW   rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis;
KW   Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW   systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW   transplant rejection; graft versus host disease; pemphigus vulgaris;
KW   glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW   irritable bowel disease; Sjogren's syndrome.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200187338-A1.
XX
PD   22-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-US015626.
XX
PR   12-MAY-2000; 2000EP-00110063.
PR   06-OCT-2000; 2000US-0238762P.
XX
PA   (GPCB-) GPC BIOTECH AG.
PA   (MORP-) MORPHOSYS AG.
XX
PI   Nagy Z,  Tesar M,  Thomassen-Wolf E;
XX
DR   WPI; 2002-075289/10.
XX
PT   Composition for suppressing immune response, treating diseases of immune
PT   system, has polypeptide comprising antibody-based antigen-binding domain
PT   of human composition, which binds antigen expressed on a cell surface.
XX
PS   Example; Page 60; 139pp; English.
XX
CC   The present invention describes a composition (I), comprising a
CC   polypeptide comprising an antibody-based antigen-binding domain of human
CC   composition with binding specificity for an antigen expressed on the
CC   surface of a cell, where treating cells expressing the antigen with the
CC   polypeptides leads to suppression of an immune response, and the IC50 for
CC   the suppression of immune response is 1 microM or less. (I) has
CC   antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC   antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC   antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
CC   can be used as a suppressor of immune response. (I) is useful for
CC   suppressing activation or proliferation of a cell of the immune system,
CC   suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC   immune system with another cell, immunosuppressing a patient and for
CC   killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC   the surface of the cell, where neither cytotoxic entities nor
CC   immunological mechanisms are needed to cause or lead to the killing. (I)
CC   (optionally linked to cytotoxic or immunogenic agent) is useful for
CC   preparing a pharmaceutical preparation for the treatment of rheumatoid
CC   arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC   insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC   erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC   host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC   glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary
CC   cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC   ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC   the exemplification of the present invention
XX
SQ   Sequence 12 AA;

  Query Match             100.0%;  Score 53;  DB 5;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          1 RASQSVSSSYLA 12


RESULT 8
AAE38096
ID   AAE38096 standard; peptide; 12 AA.
XX
AC   AAE38096;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human COU-1 antibody VL CDR1 peptide #1.
XX
KW   Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
KW   adenocarcinoma; therapy; cancer; antibody; light chain variable region;
KW   complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO2003057168-A2.
XX
PD   17-JUL-2003.
XX
PF   03-JAN-2003; 2003WO-US000297.
XX
PR   03-JAN-2002; 2002US-0345208P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Ditzel H,  Jensenius JC;
XX
DR   WPI; 2003-598315/56.
XX
PT   Novel isolated cancer-associated epitope comprising two separate
PT   polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
PT   polypeptide, useful as component of vaccine for preventing or treating
PT   adenocarcinoma.
XX
PS   Claim 15; Page 36; 155pp; English.
XX
CC   The invention provides a cancer-associated epitope comprising two
CC   separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
CC   polypeptide. Vaccine composition of the invention is useful for treating
CC   or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
CC   adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
CC   adenocarcinoma or non-seminomal testis carcinoma. The invention is also
CC   useful for preparing a medicament for treating or preventing cancer in a
CC   mammal. The present sequence is human COU-1 cancer-associated epitope
CC   antibody VL (light chain variable region) CDR (complementarity
CC   determining region) peptide
XX
SQ   Sequence 12 AA;

  Query Match             100.0%;  Score 53;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          1 RASQSVSSSYLA 12


RESULT 9
AAE38067
ID   AAE38067 standard; peptide; 12 AA.
XX
AC   AAE38067;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human 17G1 CD30 antibody VL CDR1 peptide.
XX
KW   Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
KW   systemic lupus erythematosus; systemic sclerosis; Grave's disease; ALCL;
KW   atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
KW   acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
KW   Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
KW   adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;
```

KW Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
KW light chain variable domain; VL; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO2003059282-A2.
XX
PD 24-JUL-2003.
XX
PF 07-JAN-2003; 2003WO-US000440.
XX
PR 09-JAN-2002; 2002US-0347649P.
PR 19-AUG-2002; 2002US-0404427P.
PR 06-DEC-2002; 2002US-0431684P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Keler T, Graziano R, Treml J;
XX
DR WPI; 2003-598476/56.
DR N-PSDB; AAD57379.
XX
PT New human monoclonal antibody that binds to human CD30, useful for
PT treating or preventing tumor or autoimmune disease, e.g., rheumatoid
PT arthritis.
XX
PS Disclosure; Page 117; 122pp; English.
XX
CC The invention relates to human monoclonal antibody that binds to human
CC CD30. The antibody is useful for treating or preventing tumour or
CC autoimmune disease e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
CC Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,
CC chronic renal failure, acute infectious mononucleosis, herpes or HIV
CC (human immunodeficiency virus) virus-associated diseases. The antibody is
CC also useful for treating Hodgkin's disease, anaplastic large cell
CC lymphoma (ALCL), adult T cell lymphoma (ATL), angioimmunoblastic
CC lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity
CC based lymphomas, embryonal carcinomas, undifferentiated carcinomas of the
CC rhino-pharynx (e.g. Schmincke's tumour), Castleman's disease, Kaposi's
CC Sarcoma and other T-cell or B-cell lymphomas. The present sequence is
CC human CD30 antibody VL (light chain variable domain) CDR (complementarity
CC determining region) peptide
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 10
ADA90302
ID ADA90302 standard; peptide; 12 AA.
XX
AC ADA90302;
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #3.2 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX
DR WPI; 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Example 5; Page 64; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (I), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (I); (8) testing the resulting Fab optimisation library by panning
CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (I), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (I) has
CC neuroprotective, nootropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 11
ADA90308
ID ADA90308 standard; peptide; 12 AA.

XX
AC ADA90308;
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #3.2.H2 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX
DR WPI; 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Example 5; Page 64; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (I), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (I); (8) testing the resulting Fab optimisation library by panning
CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (I), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (I) has
CC neuroprotective, nootropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 12
ADA90317
ID ADA90317 standard; peptide; 12 AA.
XX
AC ADA90317;
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #3.4.H6 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX
DR WPI; 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Example 5; Page 64; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (I), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (I); (8) testing the resulting Fab optimisation library by panning
CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (I), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a

CC pharmaceutical composition prepared by method (8). (I) has
CC neuroprotective, nootropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 13
ADA90323
ID ADA90323 standard; peptide; 12 AA.
XX
AC ADA90323;
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #3.4.H12 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX
DR WPI; 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Example 5; Page 64; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (I), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (I); (8) testing the resulting Fab optimisation library by panning
CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (I), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (I) has
CC neuroprotective, nootropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 14
ADA90324
ID ADA90324 standard; peptide; 12 AA.
XX
AC ADA90324;
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #3.4.H13 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.

XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX
DR WPI; 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Example 5; Page 64; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (I), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (I); (8) testing the resulting Fab optimisation library by panning
CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (I), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (I) has
CC neuroprotective, nootropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

RESULT 15
ADA90641
ID ADA90641 standard; peptide; 12 AA.
XX
AC ADA90641;
XX
DT 20-NOV-2003 (first entry)
XX
DE MS-Roche #7.9.H1 L-CDR1 amino acid sequence.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070760-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
XX
PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
XX
DR WPI; 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognizing two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Example 5; Page 66; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (I), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (I); (8) testing the resulting Fab optimisation library by panning
CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (I), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (I) has
CC neuroprotective, nootropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation
CC against beta-amyloid plaque formation. In particular, the disease is
CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 1 RASQSVSSSYLA 12

Search completed: August 18, 2005, 06:09:16

Job time : 26.8657 secs

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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 4.79152 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-38
Perfect score: 53
Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	100.0	83	2	I30607	Ig kappa chain V-I
2	53	100.0	87	2	S16823	Ig kappa chain V r
3	53	100.0	89	2	S34096	Ig kappa chain V r
4	53	100.0	91	2	S37520	Ig kappa chain V r
5	53	100.0	91	2	S67940	Ig kappa chain V r
6	53	100.0	92	2	S37514	Ig kappa chain V r
7	53	100.0	92	2	S37513	Ig kappa chain V r
8	53	100.0	92	2	S37518	Ig kappa chain V r
9	53	100.0	92	2	S37517	Ig kappa chain V r
10	53	100.0	92	2	S37519	Ig kappa chain V r
11	53	100.0	93	2	S37526	Ig kappa chain V r
12	53	100.0	93	2	S37528	Ig kappa chain V r
13	53	100.0	96	2	A30601	Ig kappa chain V-I
14	53	100.0	100	1	K3HUNG	Ig kappa chain pre
15	53	100.0	104	2	PH0964	Ig kappa chain V r
16	53	100.0	107	2	PH0965	Ig kappa chain V r
17	53	100.0	108	2	H44151	Ig kappa chain V r
18	53	100.0	108	2	C30608	Ig kappa chain V-I
19	53	100.0	109	2	H30601	Ig kappa chain V-I
20	53	100.0	109	2	A30608	Ig kappa chain V-I
21	53	100.0	109	2	C30601	Ig kappa chain V-I
22	53	100.0	109	2	B30601	Ig kappa chain V-I
23	53	100.0	109	2	PH0963	Ig kappa chain V r
24	53	100.0	109	2	D30601	Ig kappa chain V-I
25	53	100.0	109	2	F30607	Ig kappa chain V-I
26	53	100.0	116	2	B27594	Ig kappa chain pre
27	53	100.0	121	2	S40327	Ig kappa chain - h
28	53	100.0	129	1	K3HUHA	Ig kappa chain pre
29	53	100.0	129	1	K3HUHI	Ig kappa chain pre
30	53	100.0	129	2	S46369	IG light chain var
31	53	100.0	134	2	S38643	Ig kappa chain V r
32	52	98.1	114	2	S46375	Ig kappa chain V-J
33	50	94.3	47	2	B30607	Ig kappa chain V-I
34	50	94.3	62	2	I30601	Ig kappa chain V-I
35	50	94.3	92	2	S37510	Ig kappa chain V r
36	50	94.3	96	2	S45441	Ig kappa chain V r
37	50	94.3	109	1	K3HUSI	Ig kappa chain V-I
38	50	94.3	116	2	S41817	Ig kappa chain V r
39	50	94.3	116	2	C27594	Ig kappa chain pre
40	50	94.3	119	2	S41816	Ig kappa chain V r
41	49	92.5	87	2	S16843	Ig kappa chain V r
42	49	92.5	92	2	S37524	Ig kappa chain V r
43	49	92.5	93	2	S37508	Ig kappa chain V r
44	49	92.5	109	1	K3HUPM	Ig kappa chain V-I
45	49	92.5	110	2	S44120	Ig kappa chain V-J

ALIGNMENTS

RESULT 1
I30607
Ig kappa chain V-III region (Wei) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C;Accession: I30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: I30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-83 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 24 RASQSVSSSYLA 35

RESULT 2
S16823
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16823
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16823
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-87 <BLA>
A;Cross-references: EMBL:X54821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
||||||||||||
Db 15 RASQSVSSSYLA 26

```
RESULT 3
S34096
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34096
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <WAG>
A;Cross-references: UNIPROT:Q9UL78; EMBL:X67180
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-84/Domain: immunoglobulin homology <IMM>

  Query Match            100.0%;  Score 53;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         17 RASQSVSSSYLA 28


RESULT 4
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37520
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>
A;Cross-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405683
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match            100.0%;  Score 53;  DB 2;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          7 RASQSVSSSYLA 18


RESULT 5
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A;Reference number: S67940; MUID:92314301; PMID:1617110
A;Accession: S67940
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <HEX>
A;Cross-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology

  Query Match            100.0%;  Score 53;  DB 2;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          5 RASQSVSSSYLA 16


RESULT 6
S37514
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37514
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood,
A;Reference number: S37501
A;Accession: S37514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PID:g405671
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match            100.0%;  Score 53;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          7 RASQSVSSSYLA 18


RESULT 7
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood,
A;Reference number: S37501
A;Accession: S37513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match            100.0%;  Score 53;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db          7 RASQSVSSSYLA 18


RESULT 8
S37518
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37518
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood,
```

A;Reference number: S37501
A;Accession: S37518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26614; NID:g405678; PIDN:CAA81367.1; PID:g405679
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match 100.0%; Score 53; DB 2; Length 92;
  Best Local Similarity 100.0%; Pred. No. 0.0015;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 7 RASQSVSSSYLA 18

RESULT 9
S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37517
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match 100.0%; Score 53; DB 2; Length 92;
  Best Local Similarity 100.0%; Pred. No. 0.0015;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 7 RASQSVSSSYLA 18

RESULT 10
S37519
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37519
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match 100.0%; Score 53; DB 2; Length 92;
  Best Local Similarity 100.0%; Pred. No. 0.0015;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 7 RASQSVSSSYLA 18

RESULT 11
S37526
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S37526
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37526
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <KLE>
A;Cross-references: EMBL:Z26618; NID:g405694; PIDN:CAA81371.1; PID:g405695
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match 100.0%; Score 53; DB 2; Length 93;
  Best Local Similarity 100.0%; Pred. No. 0.0015;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 7 RASQSVSSSYLA 18

RESULT 12
S37528
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37528
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <KLE>
A;Cross-references: EMBL:Z26616; NID:g405698; PIDN:CAA81369.1; PID:g405699
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match 100.0%; Score 53; DB 2; Length 93;
  Best Local Similarity 100.0%; Pred. No. 0.0015;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 7 RASQSVSSSYLA 18

RESULT 13
A30601
Ig kappa chain V-III region (Kv325) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: A30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: A30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-96 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match 100.0%; Score 53; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35
```

RESULT 14
K3HUNG
Ig kappa chain precursor V-III region (NG9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01894
R;Bentley, D.L.
Nature 307, 77-80, 1984
A;Title: Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small fa
A;Reference number: A01894; MUID:84093600; PMID:6419127
A;Accession: A01894
A;Molecule type: DNA
A;Residues: 1-100 <BEN>
A;Cross-references: UNIPROT:P01621
A;Note: the sequence was determined from the germline gene
C;Comment: This gene was isolated from the NG9/9.1 hybridoma.
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F;5-100/Product: Ig kappa chain V-III region (NG9) #status predicted <MAT>
F;20-95/Domain: immunoglobulin homology <IMM>
F;27-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 53; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         28 RASQSVSSSYLA 39
```

RESULT 15
PH0964
Ig kappa chain V region (G6+ CLL-SIC) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PH0964
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0964
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-104 <MAR>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-21/Region: framework 1
F;14-89/Domain: immunoglobulin homology <IMM>
F;22-32/Region: complementarity-determining 1
F;33-48/Region: framework 2
F;49-54/Region: complementarity-determining 2
F;55-87/Region: framework 3
F;88-92/Region: complementarity-determining 3

Query Match 100.0%; Score 53; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         22 RASQSVSSSYLA 33
```

Search completed: August 18, 2005, 06:20:11
Job time : 5.79152 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 22.5159 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-38
Perfect score: 53
Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	100.0	100	1	KV3C_HUMAN	P01621 homo sapien
2	53	100.0	109	2	Q9UL78	Q9ul78 homo sapien
3	53	100.0	109	2	Q9UL86	Q9ul86 homo sapien
4	53	100.0	129	1	KV3L_HUMAN	P18135 homo sapien
5	53	100.0	129	1	KV3M_HUMAN	P18136 homo sapien
6	50	94.3	109	1	KV3B_HUMAN	P01620 homo sapien
7	50	94.3	236	2	Q6PIL8	Q6pil8 homo sapien
8	49	92.5	109	1	KV3F_HUMAN	P01624 homo sapien
9	49	92.5	116	1	KV3J_HUMAN	P04434 homo sapien
10	46	86.8	109	1	KV3D_HUMAN	P01622 homo sapien
11	46	86.8	235	2	Q6GMV9	Q6gmv9 homo sapien
12	45	84.9	109	1	KV3E_HUMAN	P01623 homo sapien
13	44	83.0	114	2	Q8K1F1	Q8k1f1 mus musculu
14	44	83.0	235	2	Q6PJF2	Q6pjf2 homo sapien
15	43	81.1	108	1	KV3A_HUMAN	P01619 homo sapien
16	39	73.6	129	1	KV4A_MOUSE	P01680 mus musculu
17	39	73.6	131	2	Q811C3	Q811c3 mus musculu
18	39	73.6	236	2	Q6P5S8	Q6p5s8 homo sapien
19	38.5	72.6	115	1	KV3I_HUMAN	P04433 homo sapien
20	38	71.7	447	1	G6PI_LACLA	P81181 lactococcus
21	38	71.7	449	2	Q8GQP6	Q8gqp6 streptococc
22	37	69.8	363	2	Q8XK57	Q8xk57 clostridium
23	37	69.8	612	2	Q7R3T4	Q7r3t4 giardia lam
24	36	67.9	160	2	Q6LR05	Q6lr05 photobacter
25	36	67.9	1052	2	Q6PCR6	Q6pcr6 brachydanio
26	35	66.0	101	2	Q9JL78	Q9jl78 mus musculu
27	35	66.0	108	1	KV3V_MOUSE	P01674 mus musculu
28	35	66.0	108	2	Q9UL83	Q9ul83 homo sapien
29	35	66.0	124	2	Q8C3A7	Q8c3a7 mus musculu
30	35	66.0	128	1	KV3K_HUMAN	P06311 homo sapien
31	35	66.0	195	2	Q8G9K4	Q8g9k4 streptococc
32	35	66.0	238	2	Q66JS7	Q66js7 mus musculu
33	35	66.0	388	2	Q9J871	Q9j871 spodoptera
34	35	66.0	449	1	G6PI_STRA3	P64195 streptococc
35	35	66.0	449	1	G6PI_STRA5	P64196 streptococc
36	35	66.0	449	1	G6PI_STRMU	Q9x670 streptococc
37	35	66.0	449	1	G6PI_STRP3	Q8k8q6 streptococc
38	35	66.0	449	1	G6PI_STRP8	Q8p2r3 streptococc
39	35	66.0	449	1	G6PI_STRPN	Q97ng0 streptococc
40	35	66.0	449	1	G6PI_STRPY	Q9a1l1 streptococc
41	35	66.0	449	1	G6PI_STRR6	Q8dn74 streptococc
42	35	66.0	449	1	G6PI_STRTR	Q8vvb7 streptococc
43	35	66.0	449	2	Q8RP79	Q8rp79 streptococc
44	35	66.0	449	2	Q835G1	Q835g1 enterococcu
45	35	66.0	461	2	Q6N7X2	Q6n7x2 rhodopseudo

ALIGNMENTS

RESULT 1
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RT a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.
DR PIR; A01894; K3HUNG.
DR HSSP; P01625; 1EEQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 Ig kappa chain V-III region NG9.
FT DISULFID 27 93 By similarity.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         28 RASQSVSSSYLA 39
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RESULT 2
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; H44151; H44151.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0964; PH0964.
DR   PIR; PH0965; PH0965.
DR   PIR; S33988; S33988.
DR   PIR; S34096; S34096.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             100.0%;  Score 53;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 3
Q9UL86
ID   Q9UL86      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -.
DR   PIR; B30607; B30607.
DR   PIR; I30601; I30601.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;

  Query Match             100.0%;  Score 53;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         24 RASQSVSSSYLA 35


RESULT 4
KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig kappa chain V-III region HAH.
FT   DOMAIN       21     43       Framework-1.
FT   DOMAIN       44     55       Complementarity-determining-1.
FT   DOMAIN       56     70       Framework-2.
FT   DOMAIN       71     77       Complementarity-determining-2.
FT   DOMAIN       78    109       Framework-3.
FT   DOMAIN      110    118       Complementarity-determining-3.
FT   DOMAIN      119    129       JK1 segment.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             100.0%;  Score 53;  DB 1;  Length 129;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.0082;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         44 RASQSVSSSYLA 55


RESULT 5
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0021; K3HUHI.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig kappa chain V-III region HIC.
FT   DOMAIN       21     43       Framework-1.
FT   DOMAIN       44     55       Complementarity-determining-1.
FT   DOMAIN       56     70       Framework-2.
FT   DOMAIN       71     77       Complementarity-determining-2.
FT   DOMAIN       78    109       Framework-3.
FT   DOMAIN      110    118       Complementarity-determining-3.
FT   DOMAIN      119    129       JK1 segment.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14070 MW;  7395528EA2BB74D6 CRC64;

  Query Match             100.0%;  Score 53;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 0.0082;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              ||||||||||||
Db         44 RASQSVSSSYLA 55


RESULT 6
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01892; K3HUSI.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match              94.3%;  Score 50;  DB 1;  Length 109;
  Best Local Similarity    91.7%;  Pred. No. 0.028;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              |||||||:||||
Db         24 RASQSVSNSYLA 35


RESULT 7
Q6PIL8
ID   Q6PIL8      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032451; AAH32451.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match             94.3%;  Score 50;  DB 2;  Length 236;
  Best Local Similarity   91.7%;  Pred. No. 0.069;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              |||||:||||||
Db         44 RASQSLSSSYLA 55


RESULT 8
KV3F_HUMAN
ID   KV3F_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01624;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region POM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76276460; PubMed=60899;
RA   Klapper D.G., Capra J.D.;
RT   "The amino acid sequence of the variable regions of the light chains
RT   from two idiotypically cross reactive IgM anti-gamma globulins.";
RL   Ann. Immunol. (Paris) 127C:261-271(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01897; K3HUPM.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11922 MW;  62821DDC6A8ABA86 CRC64;

  Query Match             92.5%;  Score 49;  DB 1;  Length 109;
  Best Local Similarity   83.3%;  Pred. No. 0.046;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              |||||:|:||||
Db         24 RASQSISNSYLA 35


RESULT 9
KV3J_HUMAN
ID   KV3J_HUMAN     STANDARD;      PRT;   116 AA.
AC   P04434;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region VH precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85087932; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated within
RT   the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR   PIR; A01901; K3HUVH.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21   >116       Ig kappa chain V-III region VH.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     55       Complementarity-determining-1.
FT   DOMAIN      56     70       Framework-2.
FT   DOMAIN      71     77       Complementarity-determining-2.
FT   DOMAIN      78    109       Framework-3.
FT   DOMAIN     110    116       Complementarity-determining-3.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    116    116
SQ   SEQUENCE   116 AA;  12757 MW;  51CD55BA53B21929 CRC64;

  Query Match             92.5%;  Score 49;  DB 1;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYL 11
              |||||||||||
Db         44 RASQSVSSSYL 54


RESULT 10
KV3D_HUMAN
ID   KV3D_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01622;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region Ti.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   Ti). IV. The complete amino acid sequence and its significance for the
RT   mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01895; K3HUTI.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11788 MW;  8C35058CDC7749BC CRC64;

  Query Match             86.8%;  Score 46;  DB 1;  Length 109;
  Best Local Similarity   83.3%;  Pred. No. 0.19;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              |||||||:|:||
Db         24 RASQSVSNSFLA 35


RESULT 11
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             86.8%;  Score 46;  DB 2;  Length 235;
  Best Local Similarity   83.3%;  Pred. No. 0.47;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              |||||||:|:||
Db         44 RASQSVNSKYLA 55


RESULT 12
KV3E_HUMAN
ID   KV3E_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01623;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region WOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11746 MW;  566C115E6B9CBEEE CRC64;

  Query Match             84.9%;  Score 45;  DB 1;  Length 109;
  Best Local Similarity   90.9%;  Pred. No. 0.31;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYL 11
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                ||||||||  ||
Db          24 RASQSVSSGYL 34


RESULT 13
Q8K1F1
ID   Q8K1F1      PRELIMINARY;      PRT;   114 AA.
AC   Q8K1F1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-VIPase light chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA   Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF516284; AAM64202.1; -.
DR   PIR; A33933; A33933.
DR   PIR; PH1058; PH1058.
DR   HSSP; P01837; 25C8.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12162 MW;  8BD9833DBF3EEFD1 CRC64;

  Query Match             83.0%;  Score 44;  DB 2;  Length 114;
  Best Local Similarity   90.9%;  Pred. No. 0.52;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYL 11
              ||| |||||||
Db         24 RASSSVSSSYL 34


RESULT 14
Q6PJF2
ID   Q6PJF2      PRELIMINARY;      PRT;   235 AA.
AC   Q6PJF2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016380; AAH16380.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match             83.0%;  Score 44;  DB 2;  Length 235;
  Best Local Similarity   83.3%;  Pred. No. 1.2;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
              |||| |||:|||
Db         44 RASQIVSSAYLA 55


RESULT 15
KV3A_HUMAN
ID   KV3A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01619;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-III region B6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   PubMed=11946339;
RA   Milstein C.;
RT   "The basic sequences of immunoglobulin kappa chains: sequence studies
RT   of Bence Jones proteins Rad, Fr4 and B6.";
RL   FEBS Lett. 2:301-304(1969).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01891; K3HUB6.
DR   HSSP; P01625; 1EEQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11635 MW;  8BC14FF07A419E3D CRC64;

  Query Match             81.1%;  Score 43;  DB 1;  Length 108;
  Best Local Similarity   75.0%;  Pred. No. 0.8;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASQSVSSSYLA 12
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Db 24 RASQSLSGNYLA 35

Search completed: August 18, 2005, 06:18:17
Job time : 23.5159 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 22.7279 Seconds
(without alignments)
206.752 Million cell updates/sec

Title: US-10-684-957-38
Perfect score: 53
Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	53	100.0	12	9	US-09-828-708-38	Sequence 38, Appl
2	53	100.0	12	9	US-09-828-708-40	Sequence 40, Appl
3	53	100.0	12	9	US-09-828-708-41	Sequence 41, Appl
4	53	100.0	12	9	US-09-828-708-42	Sequence 42, Appl
5	53	100.0	12	10	US-09-563-222-11	Sequence 11, Appl
6	53	100.0	12	14	US-10-001-934-62	Sequence 62, Appl
7	53	100.0	12	15	US-10-374-932-8	Sequence 8, Appli
8	53	100.0	12	15	US-10-338-366-20	Sequence 20, Appl
9	53	100.0	12	15	US-10-275-046-19	Sequence 19, Appl
10	53	100.0	12	15	US-10-379-741-8	Sequence 8, Appli
11	53	100.0	12	16	US-10-663-244-30	Sequence 30, Appl
12	53	100.0	12	16	US-10-714-353-38	Sequence 38, Appl
13	53	100.0	12	16	US-10-783-950-11	Sequence 11, Appl
14	53	100.0	12	17	US-10-684-957-38	Sequence 38, Appl
15	53	100.0	12	17	US-10-783-311-304	Sequence 304, App
16	53	100.0	12	17	US-10-883-020-15	Sequence 15, Appl
17	53	100.0	12	17	US-10-726-332-194	Sequence 194, App
18	53	100.0	12	17	US-10-891-658-107	Sequence 107, App
19	53	100.0	12	17	US-10-891-658-113	Sequence 113, App
20	53	100.0	12	17	US-10-891-658-125	Sequence 125, App
21	53	100.0	12	17	US-10-630-009-38	Sequence 38, Appl
22	53	100.0	12	17	US-10-630-009-40	Sequence 40, Appl
23	53	100.0	12	17	US-10-630-009-41	Sequence 41, Appl
24	53	100.0	12	17	US-10-630-009-42	Sequence 42, Appl
25	53	100.0	12	17	US-10-506-743-4	Sequence 4, Appli
26	53	100.0	12	18	US-10-982-725-8	Sequence 8, Appli
27	53	100.0	12	18	US-10-505-313-96	Sequence 96, Appl
28	53	100.0	12	18	US-10-505-313-143	Sequence 143, App
29	53	100.0	12	18	US-10-505-313-211	Sequence 211, App
30	53	100.0	28	15	US-10-269-711-57	Sequence 57, Appl
31	53	100.0	28	16	US-10-684-109-68	Sequence 68, Appl
32	53	100.0	74	14	US-10-125-687-23	Sequence 23, Appl
33	53	100.0	74	18	US-10-996-191-23	Sequence 23, Appl
34	53	100.0	95	9	US-09-948-939-5	Sequence 5, Appli
35	53	100.0	95	14	US-10-041-860-371	Sequence 371, App
36	53	100.0	96	14	US-10-194-975-82	Sequence 82, Appl
37	53	100.0	96	14	US-10-153-382-22	Sequence 22, Appl
38	53	100.0	96	14	US-10-041-860-10	Sequence 10, Appl
39	53	100.0	96	14	US-10-041-860-370	Sequence 370, App
40	53	100.0	96	14	US-10-041-860-376	Sequence 376, App
41	53	100.0	96	14	US-10-041-860-377	Sequence 377, App
42	53	100.0	96	15	US-10-308-817-29	Sequence 29, Appl
43	53	100.0	96	15	US-10-309-762-35	Sequence 35, Appl
44	53	100.0	96	15	US-10-453-698-29	Sequence 29, Appl
45	53	100.0	96	15	US-10-038-591-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-828-708-38
; Sequence 38, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-38

Query Match 100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 2
US-09-828-708-40
; Sequence 40, Application US/09828708
; Patent No. US20020146753A1

; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-40

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Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 3
US-09-828-708-41
; Sequence 41, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-41

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Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 4
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; Sequence 42, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-42

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Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 5
US-09-563-222-11
; Sequence 11, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-11

Query Match 100.0%; Score 53; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 6
US-10-001-934-62
; Sequence 62, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
; TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/001,934
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-62

Query Match 100.0%; Score 53; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 7
US-10-374-932-8
; Sequence 8, Application US/10374932

; Publication No. US20030235586A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP
; CURRENT APPLICATION NUMBER: US/10/374,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-932-8

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Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 8
US-10-338-366-20
; Sequence 20, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Graziano, Robert
; APPLICANT: Treml, John
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-20

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 9
US-10-275-046-19
; Sequence 19, Application US/10275046
; Publication No. US20040019187A1
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-DR specific polypeptide
US-10-275-046-19

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Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 10
US-10-379-741-8
; Sequence 8, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP2
; CURRENT APPLICATION NUMBER: US/10/379,741
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-8

Query Match 100.0%; Score 53; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 11
US-10-663-244-30
; Sequence 30, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244

; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-30

Query Match 100.0%; Score 53; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 12
US-10-714-353-38
; Sequence 38, Application US/10714353
; Publication No. US20040170626A1
; GENERAL INFORMATION:
; APPLICANT: Schuurman, Janine
; APPLICANT: Havenith, Karin
; APPLICANT: Parren, Paul
; APPLICANT: van de Winkel, Jan
; APPLICANT: Williams, Denise Leah
; APPLICANT: Jorgen Petersen
; APPLICANT: Ole Baadsgaard
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
; FILE REFERENCE: GMI-059
; CURRENT APPLICATION NUMBER: US/10/714,353
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426690
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-714-353-38

Query Match 100.0%; Score 53; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 13
US-10-783-950-11
; Sequence 11, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-11

Query Match 100.0%; Score 53; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 14
US-10-684-957-38
; Sequence 38, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-38

Query Match 100.0%; Score 53; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
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Db 1 RASQSVSSSYLA 12

RESULT 15
US-10-783-311-304
; Sequence 304, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 304

; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-304

  Query Match 100.0%; Score 53; DB 17; Length 12;
  Best Local Similarity 100.0%; Pred. No. 0.0093;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      ||||||||||||
Db 1 RASQSVSSSYLA 12

Search completed: August 18, 2005, 07:08:04
Job time : 22.8529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 3.93286 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-41
Perfect score: 32
Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	7	4	US-09-563-222C-12	Sequence 12, Appl
2	32	100.0	56	1	US-08-162-102C-39	Sequence 39, Appl
3	32	100.0	96	4	US-09-472-087-87	Sequence 87, Appl
4	32	100.0	107	1	US-08-107-669D-14	Sequence 14, Appl
5	32	100.0	107	1	US-08-472-788A-14	Sequence 14, Appl
6	32	100.0	107	2	US-08-477-531B-14	Sequence 14, Appl
7	32	100.0	107	2	US-08-652-558-49	Sequence 49, Appl
8	32	100.0	107	2	US-08-082-842A-14	Sequence 14, Appl
9	32	100.0	107	4	US-08-635-109-5	Sequence 5, Appli
10	32	100.0	107	4	US-08-844-215-8	Sequence 8, Appli
11	32	100.0	108	1	US-07-634-278-86	Sequence 86, Appl
12	32	100.0	108	1	US-08-477-728-86	Sequence 86, Appl
13	32	100.0	108	1	US-08-474-040-86	Sequence 86, Appl
14	32	100.0	108	1	US-08-487-200-86	Sequence 86, Appl
15	32	100.0	108	1	US-08-488-113B-150	Sequence 150, App
16	32	100.0	108	1	US-08-477-484B-150	Sequence 150, App
17	32	100.0	108	2	US-08-646-360-150	Sequence 150, App
18	32	100.0	108	2	US-08-232-081B-42	Sequence 42, Appl
19	32	100.0	108	3	US-08-839-765-150	Sequence 150, App
20	32	100.0	108	3	US-09-136-389-150	Sequence 150, App
21	32	100.0	108	3	US-08-484-537-86	Sequence 86, Appl
22	32	100.0	108	3	US-09-240-274-178	Sequence 178, App
23	32	100.0	108	3	US-09-610-838-150	Sequence 150, App
24	32	100.0	108	4	US-09-711-485-150	Sequence 150, App
25	32	100.0	109	1	US-08-162-102C-24	Sequence 24, Appl
26	32	100.0	109	3	US-09-025-769B-16	Sequence 16, Appl
27	32	100.0	109	4	US-08-920-100B-24	Sequence 24, Appl
28	32	100.0	109	4	US-09-490-070A-16	Sequence 16, Appl
29	32	100.0	109	4	US-09-490-153-16	Sequence 16, Appl
30	32	100.0	109	4	US-09-490-324-16	Sequence 16, Appl
31	32	100.0	109	5	PCT-US93-08786-24	Sequence 24, Appl
32	32	100.0	110	3	US-09-025-769B-30	Sequence 30, Appl
33	32	100.0	110	3	US-09-025-769B-47	Sequence 47, Appl
34	32	100.0	110	4	US-09-490-070A-30	Sequence 30, Appl
35	32	100.0	110	4	US-09-490-070A-47	Sequence 47, Appl
36	32	100.0	110	4	US-09-490-153-30	Sequence 30, Appl
37	32	100.0	110	4	US-09-490-153-47	Sequence 47, Appl
38	32	100.0	110	4	US-09-490-324-30	Sequence 30, Appl
39	32	100.0	110	4	US-09-490-324-47	Sequence 47, Appl
40	32	100.0	116	1	US-08-053-131-183	Sequence 183, App
41	32	100.0	116	2	US-08-096-762-183	Sequence 183, App
42	32	100.0	116	3	US-09-042-353-46	Sequence 46, Appl
43	32	100.0	116	3	US-08-758-417A-311	Sequence 311, App
44	32	100.0	129	2	US-08-480-774A-4	Sequence 4, Appli
45	32	100.0	139	4	US-09-472-087-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-563-222C-12
; Sequence 12, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-12

Query Match 100.0%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 2
US-08-162-102C-39
; Sequence 39, Application US/08162102C
; Patent No. 5762905
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; APPLICANT: Barbas, III, Carlos F.
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Crowe, Jr., James E.
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

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;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/162,102C
;       FILING DATE:  10-DEC-1993
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haile, Ph.D., Lisa A.
;       REGISTRATION NUMBER:  38,347
;       REFERENCE/DOCKET NUMBER:  07300/007001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 678-5070
;       TELEFAX:  (619) 678-5099
;   INFORMATION FOR SEQ ID NO:  39:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  56 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-162-102C-39

  Query Match             100.0%;  Score 32;  DB 1;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         50 GASSRAT 56


RESULT 3
US-09-472-087-87
; Sequence 87, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-87

  Query Match             100.0%;  Score 32;  DB 4;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 5.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         51 GASSRAT 57


RESULT 4
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US-08-107-669D-14
; Sequence 14, Application US/08107669D
; Patent No. 5766886
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains (as amended)
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/107,669D
;      FILING DATE:  13-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele A. Cimbala
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000001/MAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-107-669D-14

  Query Match             100.0%;  Score 32;  DB 1;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         50 GASSRAT 56


RESULT 5
US-08-472-788A-14
; Sequence 14, Application US/08472788A
; Patent No. 5770196
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,788A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/082,842
;      FILING DATE:  23-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-472-788A-14

  Query Match             100.0%;  Score 32;  DB 1;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         50 GASSRAT 56


RESULT 6
US-08-477-531B-14
; Sequence 14, Application US/08477531B
; Patent No. 5821123
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains (as amended)
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,531B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/107,669
;      FILING DATE:  13-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele A. Cimbala
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000004/MAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-531B-14

  Query Match             100.0%;  Score 32;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         50 GASSRAT 56


RESULT 7
US-08-652-558-49
; Sequence 49, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-49

  Query Match             100.0%;  Score 32;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         50 GASSRAT 56
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RESULT 8
US-08-082-842A-14
; Sequence 14, Application US/08082842A
; Patent No. 5869619
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/082,842A
;      FILING DATE:  23-JUN-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-082-842A-14

  Query Match             100.0%;  Score 32;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         50 GASSRAT 56


RESULT 9
US-08-635-109-5
; Sequence 5, Application US/08635109
; Patent No. 6538114
;  GENERAL INFORMATION:
;    APPLICANT:  Persson, Mats A. A.
;    APPLICANT:  Allander, Tobias E.
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
;    TITLE OF INVENTION:  HEPATITIS C VIRUS (HCV) E2 ANTIGEN
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  REED & ROBINS
;      STREET:  285 Hamilton Avenue, Suite 200
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/635,109
;      FILING DATE:  19-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCracken, Thomas P
;      REGISTRATION NUMBER:  38,548
;      REFERENCE/DOCKET NUMBER:  2300-6146
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 327-3400
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-635-109-5

  Query Match             100.0%;  Score 32;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
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Db         50 GASSRAT 56


RESULT 10
US-08-844-215-8
; Sequence 8, Application US/08844215
; Patent No. 6747136
;  GENERAL INFORMATION:
;    APPLICANT:  PERSSON, MATS AXEL
;    APPLICANT:  ALLANDER, TOBIAS ERIK
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
;    TITLE OF INVENTION:  HEPATITIS C VIRUS (HCV) E2 ANTIGEN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBINS & ASSOCIATES
;      STREET:  90 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/844,215
;      FILING DATE:  17-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/635,109
;      FILING DATE:  19-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MCCRACKEN, THOMAS P.
;      REGISTRATION NUMBER:  38,548
;      REFERENCE/DOCKET NUMBER:  80146.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 325-7812
;      TELEFAX:  (650) 325-7823
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-844-215-8

  Query Match             100.0%;  Score 32;  DB 4;  Length 107;
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Qy          1 GASSRAT 7
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Db         50 GASSRAT 56


RESULT 11
US-07-634-278-86
; Sequence 86, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  86:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-86

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Qy          1 GASSRAT 7
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Db         51 GASSRAT 57


RESULT 12
US-08-477-728-86
; Sequence 86, Application US/08477728
; Patent No. 5585089
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  86:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-86

  Query Match             100.0%;  Score 32;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         51 GASSRAT 57


RESULT 13
US-08-474-040-86
; Sequence 86, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
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;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  86:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-86

  Query Match             100.0%;  Score 32;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
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Db         51 GASSRAT 57


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; Sequence 86, Application US/08487200
; Patent No. 5693762
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,200
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  86:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-487-200-86

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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         51 GASSRAT 57


RESULT 15
US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
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;     CURRENT APPLICATION DATA:
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;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/425,336
;       FILING DATE:  18-APR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  150:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  108 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-488-113B-150

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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
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Db         51 GASSRAT 57


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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Title: US-10-684-957-41
Perfect score: 32
Sequence: 1 GASSRAT 7

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	7	9	US-09-948-939-30	Sequence 30, Appl
2	32	100.0	7	9	US-09-828-708-45	Sequence 45, Appl
3	32	100.0	7	9	US-09-828-708-47	Sequence 47, Appl
4	32	100.0	7	9	US-09-828-708-48	Sequence 48, Appl
5	32	100.0	7	9	US-09-828-708-49	Sequence 49, Appl
6	32	100.0	7	10	US-09-563-222-12	Sequence 12, Appl
7	32	100.0	7	10	US-09-791-153A-7	Sequence 7, Appli
8	32	100.0	7	15	US-10-338-366-22	Sequence 22, Appl
9	32	100.0	7	16	US-10-663-244-31	Sequence 31, Appl
10	32	100.0	7	16	US-10-312-316-30	Sequence 30, Appl
11	32	100.0	7	16	US-10-714-353-21	Sequence 21, Appl
12	32	100.0	7	16	US-10-714-353-27	Sequence 27, Appl
13	32	100.0	7	16	US-10-714-353-33	Sequence 33, Appl
14	32	100.0	7	16	US-10-714-353-39	Sequence 39, Appl
15	32	100.0	7	16	US-10-783-950-12	Sequence 12, Appl
16	32	100.0	7	17	US-10-684-957-41	Sequence 41, Appl
17	32	100.0	7	17	US-10-783-311-233	Sequence 233, App
18	32	100.0	7	17	US-10-783-311-305	Sequence 305, App
19	32	100.0	7	17	US-10-883-020-22	Sequence 22, Appl
20	32	100.0	7	17	US-10-726-332-147	Sequence 147, App
21	32	100.0	7	17	US-10-726-332-162	Sequence 162, App
22	32	100.0	7	17	US-10-726-332-195	Sequence 195, App
23	32	100.0	7	17	US-10-891-658-102	Sequence 102, App
24	32	100.0	7	17	US-10-891-658-114	Sequence 114, App
25	32	100.0	7	17	US-10-891-658-126	Sequence 126, App
26	32	100.0	7	17	US-10-891-658-133	Sequence 133, App
27	32	100.0	7	17	US-10-630-009-45	Sequence 45, Appl
28	32	100.0	7	17	US-10-630-009-47	Sequence 47, Appl
29	32	100.0	7	17	US-10-630-009-48	Sequence 48, Appl
30	32	100.0	7	17	US-10-630-009-49	Sequence 49, Appl
31	32	100.0	7	17	US-10-506-743-6	Sequence 6, Appli
32	32	100.0	7	18	US-10-505-313-97	Sequence 97, Appl
33	32	100.0	7	18	US-10-505-313-144	Sequence 144, App
34	32	100.0	7	18	US-10-505-313-212	Sequence 212, App
35	32	100.0	28	15	US-10-269-711-57	Sequence 57, Appl
36	32	100.0	28	16	US-10-684-109-68	Sequence 68, Appl
37	32	100.0	74	14	US-10-125-687-23	Sequence 23, Appl
38	32	100.0	74	18	US-10-996-191-23	Sequence 23, Appl
39	32	100.0	91	15	US-10-038-591-22	Sequence 22, Appl
40	32	100.0	91	16	US-10-775-444A-22	Sequence 22, Appl
41	32	100.0	95	9	US-09-948-939-5	Sequence 5, Appli
42	32	100.0	96	14	US-10-194-975-82	Sequence 82, Appl
43	32	100.0	96	14	US-10-153-382-22	Sequence 22, Appl
44	32	100.0	96	14	US-10-041-860-10	Sequence 10, Appl
45	32	100.0	96	14	US-10-041-860-370	Sequence 370, App

ALIGNMENTS

RESULT 1
US-09-948-939-30
; Sequence 30, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain CDR2 (HuMab 4B6)
US-09-948-939-30

Query Match 100.0%; Score 32; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 2
US-09-828-708-45
; Sequence 45, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-45

Query Match 100.0%; Score 32; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 3
US-09-828-708-47
; Sequence 47, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-47

Query Match 100.0%; Score 32; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 4
US-09-828-708-48
; Sequence 48, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-48

Query Match 100.0%; Score 32; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
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Db 1 GASSRAT 7

RESULT 5
US-09-828-708-49
; Sequence 49, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particip
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-49

Query Match 100.0%; Score 32; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 6
US-09-563-222-12
; Sequence 12, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-12

Query Match 100.0%; Score 32; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 7
US-09-791-153A-7
; Sequence 7, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
;  APPLICANT: Deshpande, Rajendra
;  APPLICANT:  Hitz, Anna
;  APPLICANT:  Boyle, William
;  APPLICANT:  Sullivan, John
;  TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
;  FILE REFERENCE: A-633A
;  CURRENT APPLICATION NUMBER: US/09/791,153A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: 09/511,139
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-153A-7

  Query Match             100.0%;  Score 32;  DB 10;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 8
US-10-338-366-22
; Sequence 22, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Graziano, Robert
;  APPLICANT:  Treml, John
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
;  FILE REFERENCE: MXI-180
;  CURRENT APPLICATION NUMBER: US/10/338,366
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: US 60/347649
;  PRIOR FILING DATE: 2002-01-09
;  PRIOR APPLICATION NUMBER: US 60/404427
;  PRIOR FILING DATE: 2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/431684
;  PRIOR FILING DATE: 2002-12-06
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-338-366-22

  Query Match             100.0%;  Score 32;  DB 15;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 9
US-10-663-244-31
; Sequence 31, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
;  APPLICANT: Rondon, Isaac J.
;  APPLICANT:  Edge,  Albert
;  APPLICANT:  Kent, Rachel Baribault
;  TITLE OF INVENTION: CD44 LIGANDS
;  FILE REFERENCE: 10280-063001
;  CURRENT APPLICATION NUMBER: US/10/663,244
;  CURRENT FILING DATE:  2003-09-15
;  PRIOR APPLICATION NUMBER: US 60/410,758
;  PRIOR FILING DATE: 2002-09-13
;  PRIOR APPLICATION NUMBER: US 60/469,123
;  PRIOR FILING DATE: 2003-05-09
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-31

  Query Match             100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 10
US-10-312-316-30
; Sequence 30, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Devaux, Brigitte
;  APPLICANT:  Hongo, Jo-Anne S.
;  APPLICANT:  Presta, Leonard G.
;  APPLICANT:  Shelton, David L.
;  TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
;  FILE REFERENCE: GENENT.040QPC
;  CURRENT APPLICATION NUMBER: US/10/312,316
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: 60/238,319
;  PRIOR FILING DATE: 2000-10-05
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-312-316-30

  Query Match             100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 11
US-10-714-353-21
; Sequence 21, Application US/10714353
; Publication No. US20040170626A1
; GENERAL INFORMATION:
;  APPLICANT: Schuurman, Janine
```

```
;  APPLICANT:  Havenith, Karin
;  APPLICANT:  Parren, Paul
;  APPLICANT:  van de Winkel, Jan
;  APPLICANT:  Williams, Denise Leah
;  APPLICANT:  Jorgen Petersen
;  APPLICANT:  Ole Baadsgaard
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
;  FILE REFERENCE: GMI-059
;  CURRENT APPLICATION NUMBER: US/10/714,353
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/426690
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-714-353-21

  Query Match             100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 12
US-10-714-353-27
; Sequence 27, Application US/10714353
; Publication No. US20040170626A1
; GENERAL INFORMATION:
;  APPLICANT: Schuurman, Janine
;  APPLICANT:  Havenith, Karin
;  APPLICANT:  Parren, Paul
;  APPLICANT:  van de Winkel, Jan
;  APPLICANT:  Williams, Denise Leah
;  APPLICANT:  Jorgen Petersen
;  APPLICANT:  Ole Baadsgaard
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
;  FILE REFERENCE: GMI-059
;  CURRENT APPLICATION NUMBER: US/10/714,353
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/426690
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-714-353-27

  Query Match             100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 13
US-10-714-353-33
; Sequence 33, Application US/10714353
; Publication No. US20040170626A1
; GENERAL INFORMATION:
;  APPLICANT: Schuurman, Janine
;  APPLICANT:  Havenith, Karin
;  APPLICANT:  Parren, Paul
;  APPLICANT:  van de Winkel, Jan
;  APPLICANT:  Williams, Denise Leah
;  APPLICANT:  Jorgen Petersen
;  APPLICANT:  Ole Baadsgaard
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
;  FILE REFERENCE: GMI-059
;  CURRENT APPLICATION NUMBER: US/10/714,353
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/426690
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-714-353-33

  Query Match             100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 14
US-10-714-353-39
; Sequence 39, Application US/10714353
; Publication No. US20040170626A1
; GENERAL INFORMATION:
;  APPLICANT: Schuurman, Janine
;  APPLICANT:  Havenith, Karin
;  APPLICANT:  Parren, Paul
;  APPLICANT:  van de Winkel, Jan
;  APPLICANT:  Williams, Denise Leah
;  APPLICANT:  Jorgen Petersen
;  APPLICANT:  Ole Baadsgaard
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
;  FILE REFERENCE: GMI-059
;  CURRENT APPLICATION NUMBER: US/10/714,353
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/426690
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-714-353-39

  Query Match             100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 15
US-10-783-950-12
; Sequence 12, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
;  APPLICANT: EPICYTE PHARMACEUTICALS, INC.
;  APPLICANT:  HIATT, ANDREW C.
;  APPLICANT:  HEIN, MICH B.
;  TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
;  FILE REFERENCE: 068904-0501
;  CURRENT APPLICATION NUMBER: US/10/783,950
;  CURRENT FILING DATE:  2004-02-19
```

```
;  PRIOR APPLICATION NUMBER: US/09/563,222
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: PCT/US01/14349
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 09/563,222
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-783-950-12

  Query Match            100.0%;  Score 32;  DB 16;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


Search completed: August 18, 2005, 07:08:04
Job time : 13.3829 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 15.0883 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-41
Perfect score: 32
Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	7	3	AAB52198	Aab52198 Human ant
2	32	100.0	7	4	AAU08351	Aau08351 Antibody
3	32	100.0	7	4	AAB67499	Aab67499 Human lig
4	32	100.0	7	5	AAU81258	Aau81258 Human trk
5	32	100.0	7	5	ABP62367	Abp62367 Human imm
6	32	100.0	7	5	ABP62390	Abp62390 Human imm
7	32	100.0	7	5	ABP62368	Abp62368 Human imm
8	32	100.0	7	5	ABP62372	Abp62372 Human imm
9	32	100.0	7	5	ABP62362	Abp62362 Human imm
10	32	100.0	7	5	ABP62388	Abp62388 Human imm
11	32	100.0	7	5	ABP62453	Abp62453 Human imm
12	32	100.0	7	5	ABP62387	Abp62387 Human imm
13	32	100.0	7	5	ABP62385	Abp62385 Human imm
14	32	100.0	7	5	ABP62450	Abp62450 Human imm
15	32	100.0	7	5	ABP62366	Abp62366 Human imm
16	32	100.0	7	5	ABP62381	Abp62381 Human imm
17	32	100.0	7	5	ABP62373	Abp62373 Human imm
18	32	100.0	7	5	ABP62379	Abp62379 Human imm
19	32	100.0	7	5	ABP62454	Abp62454 Human imm
20	32	100.0	7	5	ABP62360	Abp62360 Human imm
21	32	100.0	7	5	ABP62384	Abp62384 Human imm
22	32	100.0	7	5	ABP62386	Abp62386 Human imm
23	32	100.0	7	5	ABP62371	Abp62371 Human imm
24	32	100.0	7	5	ABP62389	Abp62389 Human imm
25	32	100.0	7	5	ABP62451	Abp62451 Human imm
26	32	100.0	7	5	ABP62374	Abp62374 Human imm
27	32	100.0	7	5	ABP62452	Abp62452 Human imm
28	32	100.0	7	5	ABP62455	Abp62455 Human imm
29	32	100.0	7	5	AAU70332	Aau70332 Human Kap
30	32	100.0	7	6	AAE38103	Aae38103 Human COU
31	32	100.0	7	6	AAE38068	Aae38068 Human 17G
32	32	100.0	7	6	ADA90337	Ada90337 MS-Roche
33	32	100.0	7	6	ADA90354	Ada90354 MS-Roche
34	32	100.0	7	6	ADA90499	Ada90499 MS-Roche
35	32	100.0	7	6	ADA90771	Ada90771 MS-Roche
36	32	100.0	7	6	ADA90878	Ada90878 MS-Roche
37	32	100.0	7	6	ADA90958	Ada90958 MS-R Fab/
38	32	100.0	7	6	ADA90976	Ada90976 MS-R Fab/
39	32	100.0	7	6	ADA91242	Ada91242 MS-R Fab/
40	32	100.0	7	6	ADA91355	Ada91355 MS-R Fab/
41	32	100.0	7	6	ADA90338	Ada90338 MS-Roche
42	32	100.0	7	6	ADA90506	Ada90506 MS-Roche
43	32	100.0	7	6	ADA90513	Ada90513 MS-Roche
44	32	100.0	7	6	ADA90647	Ada90647 MS-Roche
45	32	100.0	7	6	ADA90655	Ada90655 MS-Roche

ALIGNMENTS

RESULT 1
AAB52198
ID AAB52198 standard; peptide; 7 AA.
XX
AC AAB52198;
XX
DT 22-FEB-2001 (first entry)
XX
DE Human anti-HBs antibody heavy chain CDR-2 peptide SEQ ID 16.
XX
KW Anti-hepatitis B monoclonal antibody; human; hepatitis B; prevention;
KW antiinflammatory; hepatotrophic.
XX
OS Homo sapiens.
XX
PN JP2000253878-A.
XX
PD 19-SEP-2000.
XX
PF 09-MAR-1999; 99JP-00061930.
XX
PR 09-MAR-1999; 99JP-00061930.
XX
PA (NISN) NISSHINBO IND INC.
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
DR WPI; 2000-675345/66.
XX
PT Novel anti-hepatitis B monoclonal antibody used for the prevention of
PT hepatitis B.
XX
PS Claim 11; Page 13; 27pp; Japanese.
XX
CC This invention relates to a human anti-hepatitis B monoclonal antibody.
CC Included in the invention are polynucleotide sequences AAC96948 -
CC AAC96955 which encode fragments of the heavy and light chains of the
CC antibody. Proteins and peptides represented by sequences AAB52185 -
CC AAB52210 are fragments of the anti-hepatitis B light and heavy chains.
CC Also included in the invention are PCR primers AAC96956 - AAC96977 which
CC are used in the construction of the antibody. The antibody exhibits
CC antiinflammatory, and hepatotrophic activity, and can be used in a drug
CC effective at preventing hepatitis B infection
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7
```

RESULT 2
AAU08351
ID AAU08351 standard; peptide; 7 AA.
XX
AC AAU08351;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antibody light chain variable region CDR2 #3.
XX
KW Antibody; light chain; CDR2; complementarity determining region; OPGbp;
KW osteopathic; osteoprotegrin binding protein; osteoclast formation;
KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
KW bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
KW steroid-induced osteoporosis.
XX
OS Synthetic.
XX
PN WO200162932-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005973.
XX
PR 23-FEB-2000; 2000US-00511139.
PR 22-FEB-2001; 2001US-00791153.
XX
PA (AMGE-) AMGEN INC.
XX
PI Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;
XX
DR WPI; 2001-557706/62.
XX
PT Antibodies that bind antagonistically to osteoprotegrin binding protein,
PT useful for treating osteoporosis, metastasis of cancer to bone,
PT rheumatoid arthritis, hypercalcemia of malignancy and steroid-induced
PT osteoporosis.
XX
PS Claim 14; Page 129; 239pp; English.
XX
CC The invention relates to an antibody or antigen binding domain (or
CC fragment, variant or derivative), which binds to an osteoprotegrin
CC binding protein (OPGbp) and which is an antagonistic antibody. The
CC antibody or antigen binding domain may be administered to inhibit
CC osteoclast formation or activation, inhibit bone resorption in a mammal,
CC prevent or treat loss of bone mass in a mammal and to prevent or treat
CC tumour cell growth in bone. The loss of bone mass results from
CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC present sequence is an antibody light chain variable region
CC complementarity determining region, CDR2, which can be incorporated into
CC an antibody/antigen binding domain of the invention
XX
SQ Sequence 7 AA;

```
  Query Match             100.0%;  Score 32;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7
```

RESULT 3
AAB67499
ID AAB67499 standard; peptide; 7 AA.
XX
AC AAB67499;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human light chain complementarity determining region 2 (CDR2).
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023356.
XX
PR 24-AUG-1999; 99US-0150452P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX
PT Novel human sequence antibody that binds to human cytotoxic T lymphocyte
PT associated antigen-4, useful for inducing, augmenting or prolonging
PT immune response to antigen or for suppressing immune response in patient.
XX
PS Claim 31; Page 100; 127pp; English.
XX
CC AAB67490-99 and AAB67501-06 represents complementarity determining
CC regions (CDRs) of human antibodies. The antibodies specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging an
CC immune response to an antigen in a patient, where the antibodies block
CC binding of human CTLA-4 to human B7 ligands. The antibodies are also
CC useful for treating autoimmune disease in a subject caused or exacerbated
CC by increased activity of T cells and for treating prostate cancer,
CC melanoma or epithelial cancer. A polyvalent or polyclonal antibody
CC preparation comprising two antibodies of the invention are useful for
CC suppressing a immune response in a patient. They are used for treating
CC cancer, infectious diseases and promoting beneficial autoimmune reactions
CC for the treatment of diseases with inflammatory or allergic components.
CC The polyvalent or polyclonal preparations are useful for treating
CC autoimmune diseases such as rheumatoid arthritis, myasthenia gravis and
CC lupus erythematosus, multiple sclerosis, insulin-dependent diabetes
CC mellitus, transplant rejection, and inflammation, graft versus host
CC disease
XX
SQ Sequence 7 AA;

```
  Query Match             100.0%;  Score 32;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7
```

RESULT 4
AAU81258
ID AAU81258 standard; peptide; 7 AA.
XX
AC AAU81258;
XX
DT 09-APR-2002 (first entry)

XX
DE Human trkC antibody light chain CDR2 of variable region #3.
XX
KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;
KW basopaenia; lymphopaenia; monocytopaenia; neutropaenia; cancer; ulcer;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
KW cellular degeneration; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200198361-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020153.
XX
PR 22-JUN-2000; 2000US-0213141P.
PR 05-OCT-2000; 2000US-0238319P.
XX
PA (GETH) GENENTECH INC.
XX
PI Devaux B, Hongo JS, Presta LG, Shelton DL;
XX
DR WPI; 2002-130790/17.
XX
PT Novel anti-trkC agonist monoclonal antibody useful for treating
PT neurodegenerative disease, shows no significant cross-reactivity with
PT trkA/trkB, and recognizes epitope in domain 5 of trkC.
XX
PS Claim 13; Fig 11; 121pp; English.
XX
CC The invention relates to an anti-trkC agonist monoclonal antibody which
CC shows no significant cross-reactivity with trkA or trkB, and recognizes
CC an epitope in domain 5 of trkC. The antibodies of the invention are
CC effective in the treatment of cisplatin- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
CC cells such as leukopaenia including eosinopaenia, basopaenia,
CC lymphopaenia, monocytopaenia, neutropaenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
CC human and mouse anti-trkC agonist monoclonal antibodies and antibody
CC fragments of the invention
XX
SQ Sequence 7 AA;

```
  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7
```

RESULT 5
ABP62367
ID ABP62367 standard; peptide; 7 AA.
XX
AC ABP62367;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #44.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificty for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;

```
  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7
```

RESULT 6
ABP62390
ID ABP62390 standard; peptide; 7 AA.
XX
AC ABP62390;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #67.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX

PA (SCRI) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificty for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 7
ABP62368
ID ABP62368 standard; peptide; 7 AA.
XX
AC ABP62368;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #45.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificty for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 1 GASSRAT 7

RESULT 8
ABP62372
ID ABP62372 standard; peptide; 7 AA.
XX
AC ABP62372;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #49.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificty for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7

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              |||||||
Db          1 GASSRAT 7


RESULT 9
ABP62362
ID   ABP62362 standard; peptide; 7 AA.
XX
AC   ABP62362;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV E2 glycoprotein light chain CDR #39.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 10
ABP62388
ID   ABP62388 standard; peptide; 7 AA.
XX
AC   ABP62388;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV E2 glycoprotein light chain CDR #65.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 11
ABP62453
ID   ABP62453 standard; peptide; 7 AA.
XX
AC   ABP62453;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV NS 3 light chain CDR #115.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
```

```
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 12
ABP62387
ID   ABP62387 standard; peptide; 7 AA.
XX
AC   ABP62387;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV E2 glycoprotein light chain CDR #64.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 13
ABP62385
ID   ABP62385 standard; peptide; 7 AA.
XX
AC   ABP62385;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV E2 glycoprotein light chain CDR #62.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7
```

```
RESULT 14
ABP62450
ID   ABP62450 standard; peptide; 7 AA.
XX
AC   ABP62450;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV NS 3 light chain CDR #112.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


RESULT 15
ABP62366
ID   ABP62366 standard; peptide; 7 AA.
XX
AC   ABP62366;
XX
DT   10-OCT-2002  (first entry)
XX
DE   Human immunopeptide to HCV E2 glycoprotein light chain CDR #43.
XX
KW   Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW   nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW   NS3 protein; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200259340-A1.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002303.
XX
PR   26-JAN-2001; 2001US-0264451P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Maruyama T,  Jones IM,  Burton DR,  Fox RI;
XX
DR   WPI; 2002-599801/64.
XX
PT   New human immunopolypeptide with binding specificity for certain envelope
PT   glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT   diagnosing or treating patients having or suspected of having HCV
PT   infection.
XX
PS   Claim 1; Fig 17; 308pp; English.
XX
CC   The present invention relates to human immunopolypeptides, produced by a
CC   phage transfected cell library. The present sequence is one such
CC   immunopolypeptide. The immunopolypeptides have binding specificty for
CC   envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC   virus (HCV). E2 glycoprotein is believed to be responsible for target
CC   cell binding and contains neutralising epitopes, while NS3 is thought to
CC   be involved in the replication of HCV. The immunopolypeptides are useful
CC   for diagnosing and treating a patient having or suspected to be having
CC   HCV infection
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 32;  DB 5;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db          1 GASSRAT 7


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Job time : 16.0883 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 2.79505 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-41
Perfect score: 32
Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	34	2	H30607	Ig kappa chain V-I
2	32	100.0	54	2	S40381	Ig kappa chain V-I
3	32	100.0	54	2	A25521	Ig kappa chain V r
4	32	100.0	62	2	I30601	Ig kappa chain V-I
5	32	100.0	83	2	I30607	Ig kappa chain V-I
6	32	100.0	87	2	S16823	Ig kappa chain V r
7	32	100.0	87	2	S16843	Ig kappa chain V r
8	32	100.0	89	2	S34096	Ig kappa chain V r
9	32	100.0	91	2	S37520	Ig kappa chain V r
10	32	100.0	91	2	S67940	Ig kappa chain V r
11	32	100.0	92	2	S37514	Ig kappa chain V r
12	32	100.0	92	2	S37513	Ig kappa chain V r
13	32	100.0	92	2	S37510	Ig kappa chain V r
14	32	100.0	92	2	S37518	Ig kappa chain V r
15	32	100.0	92	2	S37517	Ig kappa chain V r
16	32	100.0	92	2	S37524	Ig kappa chain V r
17	32	100.0	92	2	S37519	Ig kappa chain V r
18	32	100.0	93	2	S37526	Ig kappa chain V r
19	32	100.0	93	2	S37528	Ig kappa chain V r
20	32	100.0	96	2	A30601	Ig kappa chain V-I
21	32	100.0	99	2	JH0429	Ig kappa chain V-I
22	32	100.0	104	2	PH0964	Ig kappa chain V r
23	32	100.0	107	2	PH0965	Ig kappa chain V r
24	32	100.0	108	2	H44151	Ig kappa chain V r
25	32	100.0	108	2	C30608	Ig kappa chain V-I
26	32	100.0	109	1	K3HUGO	Ig kappa chain V-I
27	32	100.0	109	1	K3HUSI	Ig kappa chain V-I
28	32	100.0	109	1	K3HUWL	Ig kappa chain V-I
29	32	100.0	109	2	S47181	Ig kappa chain - h
30	32	100.0	109	2	F30601	Ig kappa chain V-I
31	32	100.0	109	2	H30601	Ig kappa chain V-I
32	32	100.0	109	2	F44151	Ig kappa chain V r
33	32	100.0	109	2	G30607	Ig kappa chain V-I
34	32	100.0	109	2	A30608	Ig kappa chain V-I
35	32	100.0	109	2	G30601	Ig kappa chain V-I
36	32	100.0	109	2	C30601	Ig kappa chain V-I
37	32	100.0	109	2	B30601	Ig kappa chain V-I
38	32	100.0	109	2	PH0963	Ig kappa chain V r
39	32	100.0	109	2	D30601	Ig kappa chain V-I
40	32	100.0	109	2	F30607	Ig kappa chain V-I
41	32	100.0	110	2	E30607	Ig kappa chain V-I
42	32	100.0	110	2	S44120	Ig kappa chain V-J
43	32	100.0	110	2	S20635	Ig kappa chain V r
44	32	100.0	114	2	S46375	Ig kappa chain V-J
45	32	100.0	116	2	C27594	Ig kappa chain pre

ALIGNMENTS

RESULT 1
H30607
Ig kappa chain V-III region (Bla) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: H30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-34 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 4 GASSRAT 10

RESULT 2
S40381
Ig kappa chain V-III region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: S40381
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40381
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-54 <KLE>
A;Cross-references: EMBL:X72491; NID:g441450; PIDN:CAA51159.1; PID:g441451
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 9 GASSRAT 15

RESULT 3
A25521
Ig kappa chain V region (321) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997
C;Accession: A25521
R;Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, E.Y.; Schrantz, R.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986
A;Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IgM
A;Reference number: A94135; MUID:87041448; PMID:3095834
A;Accession: A25521
A;Molecule type: DNA
A;Residues: 1-54 <CHE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 9 GASSRAT 15

RESULT 4
I30601
Ig kappa chain V-III region (Boc) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: I30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: I30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-62 <GON>
A;Cross-references: UNIPROT:Q9UL86; UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 51 GASSRAT 57

RESULT 5
I30607
Ig kappa chain V-III region (Wei) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C;Accession: I30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: I30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-83 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin .

Query Match 100.0%; Score 32; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 51 GASSRAT 57

RESULT 6
S16823
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16823
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fact
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16823
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-87 <BLA>
A;Cross-references: EMBL:X54821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 42 GASSRAT 48

RESULT 7
S16843
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16843
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fact
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16843
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-87 <BLA>
A;Cross-references: EMBL:X54841
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 42 GASSRAT 48

RESULT 8
S34096
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34096
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174

A;Accession: S34096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <WAG>
A;Cross-references: UNIPROT:Q9UL78; EMBL:X67180
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 44 GASSRAT 50

RESULT 9
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37520
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>
A;Cross-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405683
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 34 GASSRAT 40

RESULT 10
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A;Reference number: S67940; MUID:92314301; PMID:1617110
A;Accession: S67940
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <HEX>
A;Cross-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 32; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 32 GASSRAT 38

RESULT 11
S37514
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37514
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PID:g405671
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 34 GASSRAT 40

RESULT 12
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 34 GASSRAT 40

RESULT 13
S37510
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37510
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37510
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26601; NID:g405662; PIDN:CAA81355.1; PID:g405663
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GASSRAT 7
              |||||||
Db         34 GASSRAT 40


RESULT 14
S37518
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37518
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26614; NID:g405678; PIDN:CAA81367.1; PID:g405679
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             100.0%;  Score 32;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         34 GASSRAT 40


RESULT 15
S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37517
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             100.0%;  Score 32;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         34 GASSRAT 40


Search completed: August 18, 2005, 06:20:11
Job time : 2.79505 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 13.1343 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-41
Perfect score: 32
Sequence: 1 GASSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	109	1	KV3B_HUMAN	P01620 homo sapien
2	32	100.0	109	1	KV3E_HUMAN	P01623 homo sapien
3	32	100.0	109	1	KV3G_HUMAN	P04206 homo sapien
4	32	100.0	109	2	Q9UL78	Q9ul78 homo sapien
5	32	100.0	129	1	KV3L_HUMAN	P18135 homo sapien
6	32	100.0	129	1	KV3M_HUMAN	P18136 homo sapien
7	32	100.0	236	2	Q6P5S8	Q6p5s8 homo sapien
8	32	100.0	256	2	Q7XZY3	Q7xzy3 oryza sativ
9	32	100.0	460	2	Q7RUN5	Q7run5 neurospora
10	32	100.0	622	2	Q7QWD2	Q7qwd2 giardia lam
11	32	100.0	975	2	Q84TI3	Q84ti3 arabidopsis
12	29	90.6	95	2	Q68986	Q68986 human endog
13	29	90.6	100	1	KV3C_HUMAN	P01621 homo sapien
14	29	90.6	107	2	Q9L0H4	Q9l0h4 streptomyce
15	29	90.6	109	1	KV3F_HUMAN	P01624 homo sapien
16	29	90.6	109	2	Q9UL85	Q9ul85 homo sapien
17	29	90.6	109	2	Q82F05	Q82f05 streptomyce
18	29	90.6	116	1	KV3J_HUMAN	P04434 homo sapien
19	29	90.6	129	1	KV3H_HUMAN	P04207 homo sapien
20	29	90.6	189	2	Q75A56	Q75a56 ashbya goss
21	29	90.6	211	2	Q92Z27	Q92z27 rhizobium m
22	29	90.6	235	2	Q6PJF2	Q6pjf2 homo sapien
23	29	90.6	316	1	CYPK_STRCO	Q02055 streptomyce
24	29	90.6	316	1	GPDA_RICPR	Q9zda0 rickettsia
25	29	90.6	319	2	Q67G32	Q67g32 streptomyce
26	29	90.6	324	2	Q8CMN2	Q8cmn2 staphylococ
27	29	90.6	335	2	Q8LCX8	Q8lcx8 arabidopsis
28	29	90.6	335	2	Q9LN63	Q9ln63 arabidopsis
29	29	90.6	335	2	Q9SEG5	Q9seg5 arabidopsis
30	29	90.6	346	2	Q9F152	Q9f152 bifidobacte
31	29	90.6	448	2	Q7UFK4	Q7ufk4 rhodopirell
32	29	90.6	537	2	Q67L80	Q67l80 symbiobacte
33	29	90.6	543	1	SRYA_DROSU	Q07965 drosophila
34	29	90.6	907	2	Q6C9S1	Q6c9s1 yarrowia li
35	29	90.6	1040	2	Q6D736	Q6d736 erwinia car
36	29	90.6	1101	2	Q82CF0	Q82cf0 streptomyce
37	29	90.6	1142	2	Q82C46	Q82c46 streptomyce
38	29	90.6	1414	1	RPOC_COXBU	Q83et0 coxiella bu
39	29	90.6	1922	2	Q7PZE8	Q7pze8 anopheles g
40	28	87.5	64	2	Q652R1	Q652r1 oryza sativ
41	28	87.5	102	2	Q9YBU5	Q9ybu5 aeropyrum p
42	28	87.5	108	1	KV3A_HUMAN	P01619 homo sapien
43	28	87.5	109	2	Q9UL86	Q9ul86 homo sapien
44	28	87.5	119	2	Q9YDK0	Q9ydk0 aeropyrum p
45	28	87.5	128	1	FLIE_RHOBA	Q7unq2 rhodopirell

ALIGNMENTS

RESULT 1
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
DR PIR; A01892; K3HUSI.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GASSRAT 7
|||||||
Db 51 GASSRAT 57

RESULT 2
KV3E_HUMAN
ID KV3E_HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-III region WOL.

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID    23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11746 MW;  566C115E6B9CBEEE CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         51 GASSRAT 57


RESULT 3
KV3G_HUMAN
ID   KV3G_HUMAN     STANDARD;      PRT;   109 AA.
AC   P04206;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region GOL (Rheumatoid factor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA   Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT   "Amino acid sequence of a light chain variable region of a human
RT   rheumatoid factor of the Wa idiotypic group, in part predicted by its
RT   reactivity with antipeptide antibodies.";
RL   Mol. Immunol. 23:239-244(1986).
DR   PIR; A01893; K3HUGO.
DR   HSSP; P01625; 1EK3.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER      109    109
SQ   SEQUENCE   109 AA;  11830 MW;  9349A5B1D93588B6 CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         51 GASSRAT 57


RESULT 4
Q9UL78
ID   Q9UL78      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; H44151; H44151.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0964; PH0964.
DR   PIR; PH0965; PH0965.
DR   PIR; S33988; S33988.
DR   PIR; S34096; S34096.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         51 GASSRAT 57


RESULT 5
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KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig kappa chain V-III region HAH.
FT   DOMAIN       21     43       Framework-1.
FT   DOMAIN       44     55       Complementarity-determining-1.
FT   DOMAIN       56     70       Framework-2.
FT   DOMAIN       71     77       Complementarity-determining-2.
FT   DOMAIN       78    109       Framework-3.
FT   DOMAIN      110    118       Complementarity-determining-3.
FT   DOMAIN      119    129       JK1 segment.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         71 GASSRAT 77


RESULT 6
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0021; K3HUHI.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig kappa chain V-III region HIC.
FT   DOMAIN       21     43       Framework-1.
FT   DOMAIN       44     55       Complementarity-determining-1.
FT   DOMAIN       56     70       Framework-2.
FT   DOMAIN       71     77       Complementarity-determining-2.
FT   DOMAIN       78    109       Framework-3.
FT   DOMAIN      110    118       Complementarity-determining-3.
FT   DOMAIN      119    129       JK1 segment.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14070 MW;  7395528EA2BB74D6 CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         71 GASSRAT 77


RESULT 7
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
```

```
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         71 GASSRAT 77


RESULT 8
Q7XZY3
ID   Q7XZY3      PRELIMINARY;      PRT;   256 AA.
AC   Q7XZY3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein OSJNBa0093M23.9 (Expressed protein).
GN   Name=OSJNBa0093M23.9; Synonyms=OSJNBa0024K17.20;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Buell R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Buell R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC138001; AAP68409.1; -.
DR   EMBL; AC145381; AAS07140.1; -.
DR   Gramene; Q7XZY3; -.
KW   Hypothetical protein.
SQ   SEQUENCE   256 AA;  28536 MW;  3B1B934F8DB73D83 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db        199 GASSRAT 205


RESULT 9
Q7RUN5
ID   Q7RUN5      PRELIMINARY;      PRT;   460 AA.
AC   Q7RUN5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein B3E4.250.
GN   Name=NCU09627.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000136; EAA34155.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   460 AA;  51343 MW;  4AC2DE4830C463FA CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 460;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db        199 GASSRAT 205


RESULT 10
Q7QWD2
ID   Q7QWD2      PRELIMINARY;      PRT;   622 AA.
AC   Q7QWD2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   GLP_336_49924_51792.
OS   Giardia lamblia ATCC 50803.
OC   Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX   NCBI_TaxID=184922;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=WB C6;
RA   Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA   Olsen G.J., Sogin M.L.;
RT   "Draft sequence of the Giardia lamblia genome.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACB01000071; EAA39390.1; -.
DR   InterPro; IPR006058; 2Fe2S_fd_BS.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_2.
SQ   SEQUENCE   622 AA;  66923 MW;  35088A1F6BA47036 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 622;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db        278 GASSRAT 284


RESULT 11
Q84TI3
ID   Q84TI3      PRELIMINARY;      PRT;   975 AA.
AC   Q84TI3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein At3g63500.
GN   Name=At3g63500;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT005768; AAO64172.1; -.
DR   InterPro; IPR004082; AraTh130.
DR   Pfam; PF07227; DUF1423; 1.
DR   PRINTS; PR01544; ARATH130DUF.
KW   Hypothetical protein.
SQ   SEQUENCE   975 AA;  109142 MW;  42CFC08F431ECF62 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||||||
Db         21 GASSRAT 27


RESULT 12
Q68986
ID   Q68986      PRELIMINARY;      PRT;    95 AA.
AC   Q68986;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Pol polyprotein (Fragment).
GN   Name=pol;
OS   Human endogenous retrovirus.
OC   Viruses; Retroid viruses; Retroviridae.
OX   NCBI_TaxID=11827;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=XA37;
RX   MEDLINE=96332499; PubMed=8760409;
RA   Widegren B., Kjellman C., Aminoff S., Sahlford L.G., Sjogren H.O.;
RT   "The structure and phylogeny of a new family of human endogenous
RT   retroviruses.";
RL   J. Gen. Virol. 77:1631-1641(1996).
DR   EMBL; U29658; AAB19069.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004523; F:ribonuclease H activity; IEA.
DR   InterPro; IPR002156; RNaseH.
DR   Pfam; PF00075; RnaseH; 1.
KW   Polyprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   95 AA;  10370 MW;  98A2CD7076DE73E2 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 95;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |:|||||
Db          8 GSSSRAT 14


RESULT 13
KV3C_HUMAN
ID   KV3C_HUMAN     STANDARD;      PRT;   100 AA.
AC   P01621;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region NG9 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093600; PubMed=6419127;
RA   Bentley D.L.;
RT   "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RT   a small family of germ-line V genes.";
RL   Nature 307:77-80(1984).
CC   -!- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.
DR   PIR; A01894; K3HUNG.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1      4
FT   CHAIN         5    100       Ig kappa chain V-III region NG9.
FT   DISULFID     27     93       By similarity.
FT   NON_TER     100    100
SQ   SEQUENCE   100 AA;  10729 MW;  5D9AF363CC52632F CRC64;

  Query Match             90.6%;  Score 29;  DB 1;  Length 100;
  Best Local Similarity   85.7%;  Pred. No. 47;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
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Db         55 GATSRAT 61


RESULT 14
Q9L0H4
ID   Q9L0H4      PRELIMINARY;      PRT;   107 AA.
AC   Q9L0H4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein SCO4783.
GN   ORFNames=SCD63.15;
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL939121; CAB82022.1; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   107 AA;  10322 MW;  F68C78C5C767E092 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 51;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              ||:||||
Db         81 GAASRAT 87


RESULT 15
KV3F_HUMAN
ID   KV3F_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01624;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region POM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76276460; PubMed=60899;
RA   Klapper D.G., Capra J.D.;
RT   "The amino acid sequence of the variable regions of the light chains
RT   from two idiotypically cross reactive IgM anti-gamma globulins.";
RL   Ann. Immunol. (Paris) 127C:261-271(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01897; K3HUPM.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11922 MW;  62821DDC6A8ABA86 CRC64;

  Query Match             90.6%;  Score 29;  DB 1;  Length 109;
  Best Local Similarity   85.7%;  Pred. No. 52;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GASSRAT 7
              |||:|||
Db         51 GASTRAT 57


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Job time : 15.1343 secs
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 4.4947 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-36
Perfect score: 46
Sequence: 1 GSYFYFDL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	87.0	139	4	US-09-248-796A-21764	Sequence 21764, A
2	36	78.3	60	4	US-09-107-433-4381	Sequence 4381, Ap
3	36	78.3	117	3	US-09-065-059-15	Sequence 15, Appl
4	36	78.3	312	4	US-09-248-796A-15104	Sequence 15104, A
5	35	76.1	117	3	US-09-157-370-2	Sequence 2, Appli
6	35	76.1	197	4	US-09-902-540-13504	Sequence 13504, A
7	35	76.1	316	3	US-08-961-083-156	Sequence 156, App
8	35	76.1	316	4	US-09-536-784-156	Sequence 156, App
9	35	76.1	332	4	US-09-583-110-3964	Sequence 3964, Ap
10	35	76.1	333	4	US-09-107-433-4789	Sequence 4789, Ap
11	35	76.1	340	4	US-09-583-110-3948	Sequence 3948, Ap
12	35	76.1	346	4	US-09-107-433-4895	Sequence 4895, Ap
13	34	73.9	72	4	US-09-270-767-58685	Sequence 58685, A
14	34	73.9	141	4	US-09-107-532A-4835	Sequence 4835, Ap
15	34	73.9	558	4	US-09-270-767-43341	Sequence 43341, A
16	34	73.9	1596	4	US-09-328-352-5542	Sequence 5542, Ap
17	33	71.7	17	4	US-09-440-781-63	Sequence 63, Appl
18	33	71.7	17	4	US-09-440-781-64	Sequence 64, Appl
19	33	71.7	17	4	US-09-440-781-66	Sequence 66, Appl
20	33	71.7	60	4	US-09-270-767-33990	Sequence 33990, A
21	33	71.7	60	4	US-09-270-767-49207	Sequence 49207, A
22	33	71.7	114	4	US-09-270-767-45468	Sequence 45468, A
23	33	71.7	177	4	US-09-248-796A-27103	Sequence 27103, A
24	33	71.7	214	4	US-09-328-352-6049	Sequence 6049, Ap
25	33	71.7	232	4	US-09-489-039A-8106	Sequence 8106, Ap
26	33	71.7	363	4	US-09-248-796A-19011	Sequence 19011, A
27	33	71.7	509	1	US-08-030-096-2	Sequence 2, Appli
28	33	71.7	540	3	US-08-687-580B-7	Sequence 7, Appli
29	33	71.7	557	4	US-09-489-039A-12479	Sequence 12479, A
30	33	71.7	559	1	US-08-030-096-6	Sequence 6, Appli
31	33	71.7	694	4	US-09-949-016-7117	Sequence 7117, Ap
32	33	71.7	811	1	US-08-480-604A-7	Sequence 7, Appli
33	33	71.7	811	2	US-08-405-496A-7	Sequence 7, Appli
34	33	71.7	811	3	US-08-915-136-7	Sequence 7, Appli
35	33	71.7	811	3	US-08-957-310-7	Sequence 7, Appli
36	33	71.7	811	4	US-10-011-366-7	Sequence 7, Appli
37	33	71.7	811	4	US-09-084-517-7	Sequence 7, Appli
38	33	71.7	812	1	US-08-480-604A-29	Sequence 29, Appl
39	33	71.7	812	3	US-08-915-136-29	Sequence 29, Appl
40	33	71.7	812	4	US-09-084-517-29	Sequence 29, Appl
41	33	71.7	866	4	US-09-545-773-2	Sequence 2, Appli
42	33	71.7	1278	4	US-09-604-957-3	Sequence 3, Appli
43	33	71.7	1475	3	US-09-007-999-2	Sequence 2, Appli
44	33	71.7	1475	3	US-09-210-361-2	Sequence 2, Appli
45	33	71.7	1475	4	US-09-740-274-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-09-248-796A-21764
; Sequence 21764, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21764
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-21764

  Query Match             87.0%;  Score 40;  DB 4;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              |||||||
Db        114 SYFYFDL 120


RESULT 2
US-09-107-433-4381
; Sequence 4381, Application US/09107433
; Patent No. 6800744
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                           SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNO
;                           THERAPEUTICS
;       NUMBER OF SEQUENCES: 5206
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
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;              COMPUTER: <Unknown>
;              OPERATING SYSTEM: <Unknown>
;              SOFTWARE: <Unknown>
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/107,433
;              FILING DATE: 30-Jun-1998
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 60/ 085131
;              FILING DATE: May 12, 1998
;              APPLICATION NUMBER: 60/051553
;              FILING DATE: July 2, 1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Ariniello, Pamela Deneke
;              REGISTRATION NUMBER: 40,489
;              REFERENCE/DOCKET NUMBER: GTC-011
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (781)893-5007
;              TELEFAX: (781)893-8277
;    INFORMATION FOR SEQ ID NO: 4381:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 60 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         HYPOTHETICAL: YES
;         ORIGINAL SOURCE:
;              ORGANISM: Streptococcus pneumoniae
;         FEATURE:
;              NAME/KEY:  misc_feature
;              LOCATION: (B) LOCATION 1...60
;         SEQUENCE DESCRIPTION: SEQ ID NO: 4381:
US-09-107-433-4381

  Query Match             78.3%;  Score 36;  DB 4;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYF 6
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Db          3 GSYFYF 8


RESULT 3
US-09-065-059-15
; Sequence 15, Application US/09065059
; Patent No. 6068841
;  GENERAL INFORMATION:
;    APPLICANT:  SEINO, Ken-ichiro
;    APPLICANT:  KAYAGAKI, No. 6068841uhiko
;    APPLICANT:  YAGITA, Hideo
;    APPLICANT:  OKUMURA, Ko
;    APPLICANT:  NAKATA, Motomi
;    TITLE OF INVENTION:  THERAPEUTIC AGENT FOR HEPATITIS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDermott, Will & Emery
;      STREET:  99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/065,059
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bucca Ph.D., Daniel
;      REGISTRATION NUMBER:  P-42,368
;      REFERENCE/DOCKET NUMBER:  50356-151
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-518-5100
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-065-059-15

  Query Match             78.3%;  Score 36;  DB 3;  Length 117;
  Best Local Similarity   71.4%;  Pred. No. 26;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              |:|:|||
Db         99 GNYYYFD 105


RESULT 4
US-09-248-796A-15104
; Sequence 15104, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15104
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-15104

  Query Match             78.3%;  Score 36;  DB 4;  Length 312;
  Best Local Similarity   75.0%;  Pred. No. 68;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFDL 8
              |||| ||:
Db        257 GSYFIFDI 264


RESULT 5
US-09-157-370-2
; Sequence 2, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
;  APPLICANT: STEIPE, Boris
;  APPLICANT: STEINBACHER, Stefan
;  TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
;  FILE REFERENCE: P8341-8072
;  CURRENT APPLICATION NUMBER: US/09/157,370A
;  CURRENT FILING DATE: 1998-09-21
;  EARLIER APPLICATION NUMBER: 08/765,179
;  EARLIER FILING DATE: 1997-01-14
;  EARLIER APPLICATION NUMBER: PCT/EP95/02626
;  EARLIER FILING DATE: 1995-07-06
;  EARLIER APPLICATION NUMBER: DE/P44 25 115.7
;  EARLIER FILING DATE: 1994-07-15
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-157-370-2

  Query Match             76.1%;  Score 35;  DB 3;  Length 117;
  Best Local Similarity   71.4%;  Pred. No. 39;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |:|||
Db         99 GGYYYFD 105


RESULT 6
US-09-902-540-13504
; Sequence 13504, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13504
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-13504

  Query Match             76.1%;  Score 35;  DB 4;  Length 197;
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Qy          1 GSYFYFDL 8
              ||::|:||
Db        153 GSWYYYDL 160


RESULT 7
US-08-961-083-156
; Sequence 156, Application US/08961083
; Patent No. 6159469
;  GENERAL INFORMATION:
;    APPLICANT:  Choi et. al.
;    TITLE OF INVENTION:  Streptococcus pneumoniae Antigens and Vaccines
;    NUMBER OF SEQUENCES:  452
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,083
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  156:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  316 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-961-083-156

  Query Match             76.1%;  Score 35;  DB 3;  Length 316;
  Best Local Similarity   71.4%;  Pred. No. 1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |:|||
Db         35 GKYYYFD 41


RESULT 8
US-09-536-784-156
; Sequence 156, Application US/09536784
; Patent No. 6573082
;   GENERAL INFORMATION:
;        APPLICANT: Choi et. al.
;        TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
;        NUMBER OF SEQUENCES: 452
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/536,784
;             FILING DATE: 30-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/961,083
;             FILING DATE: OCT-30-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Michelle S. Marks
;             REGISTRATION NUMBER: 41,971
;             REFERENCE/DOCKET NUMBER: PB340P3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (301) 309-8504
;             TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 156:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 316 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 156:
US-09-536-784-156

  Query Match             76.1%;  Score 35;  DB 4;  Length 316;
  Best Local Similarity   71.4%;  Pred. No. 1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
```

```
              | |:|||
Db          35 GKYYYFD 41


RESULT 9
US-09-583-110-3964
; Sequence 3964, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
;  APPLICANT:  Lynn Doucette-Stamm et al.
;  TITLE OF INVENTION:  Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE:  PATH00-07A
;  CURRENT APPLICATION NUMBER: US/09/583,110
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 09/107,433
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/085,131
;  PRIOR FILING DATE:  1998-05-12
;  PRIOR APPLICATION NUMBER:  US 60/051,553
;  PRIOR FILING DATE:  1997-07-02
;  NUMBER OF SEQ ID NOS:  5322
; SEQ ID NO 3964
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-3964

  Query Match             76.1%;  Score 35;  DB 4;  Length 332;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |:|||
Db         59 GKYYYFD 65


RESULT 10
US-09-107-433-4789
; Sequence 4789, Application US/09107433
; Patent No. 6800744
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                            SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNO
;                            THERAPEUTICS
;        NUMBER OF SEQUENCES: 5206
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: <Unknown>
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,433
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/ 085131
;             FILING DATE: May 12, 1998
;             APPLICATION NUMBER: 60/051553
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-011
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 4789:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 333 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: YES
;        ORIGINAL SOURCE:
;             ORGANISM: Streptococcus pneumoniae
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...333
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4789:
US-09-107-433-4789

  Query Match             76.1%;  Score 35;  DB 4;  Length 333;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |:|||
Db         60 GKYYYFD 66


RESULT 11
US-09-583-110-3948
; Sequence 3948, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
;  APPLICANT:  Lynn Doucette-Stamm et al.
;  TITLE OF INVENTION:  Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE:  PATH00-07A
;  CURRENT APPLICATION NUMBER: US/09/583,110
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 09/107,433
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/085,131
;  PRIOR FILING DATE:  1998-05-12
;  PRIOR APPLICATION NUMBER:  US 60/051,553
;  PRIOR FILING DATE:  1997-07-02
;  NUMBER OF SEQ ID NOS:  5322
; SEQ ID NO 3948
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-3948

  Query Match             76.1%;  Score 35;  DB 4;  Length 340;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |:|||
Db         59 GKYYYFD 65


RESULT 12
US-09-107-433-4895
; Sequence 4895, Application US/09107433
; Patent No. 6800744
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                            SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNOS
;                            THERAPEUTICS
;        NUMBER OF SEQUENCES: 5206
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
```

```
;              COUNTRY: USA
;              ZIP: 02354
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: CD/ROM ISO9660
;              COMPUTER: <Unknown>
;              OPERATING SYSTEM: <Unknown>
;              SOFTWARE: <Unknown>
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/107,433
;              FILING DATE: 30-Jun-1998
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 60/ 085131
;              FILING DATE: May 12, 1998
;              APPLICATION NUMBER: 60/051553
;              FILING DATE: July 2, 1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Ariniello, Pamela Deneke
;              REGISTRATION NUMBER: 40,489
;              REFERENCE/DOCKET NUMBER: GTC-011
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (781)893-5007
;              TELEFAX: (781)893-8277
;    INFORMATION FOR SEQ ID NO: 4895:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 346 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         HYPOTHETICAL: YES
;         ORIGINAL SOURCE:
;              ORGANISM: Streptococcus pneumoniae
;         FEATURE:
;              NAME/KEY:  misc_feature
;              LOCATION: (B) LOCATION 1...346
;         SEQUENCE DESCRIPTION: SEQ ID NO: 4895:
US-09-107-433-4895

  Query Match           76.1%;  Score 35;  DB 4;  Length 346;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              | |:|||
Db         65 GKYYYFD 71


RESULT 13
US-09-270-767-58685
; Sequence 58685, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58685
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58685

  Query Match           73.9%;  Score 34;  DB 4;  Length 72;
  Best Local Similarity   85.7%;  Pred. No. 36;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              ||||| |
Db         31 SYFYFSL 37


RESULT 14
US-09-107-532A-4835
; Sequence 4835, Application US/09107532A
; Patent No. 6583275
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;  INFORMATION FOR SEQ ID NO: 4835:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 141 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...141
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4835:
US-09-107-532A-4835

  Query Match           73.9%;  Score 34;  DB 4;  Length 141;
  Best Local Similarity   85.7%;  Pred. No. 70;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GSYFYFD 7
              |||| ||
Db         92 GSYFMFD 98


RESULT 15
US-09-270-767-43341
; Sequence 43341, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
```

```
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43341
;   LENGTH: 558
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43341

  Query Match            73.9%;  Score 34;  DB 4;  Length 558;
  Best Local Similarity   85.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SYFYFDL 8
              ||||| |
Db        517 SYFYFSL 523


Search completed: August 18, 2005, 06:22:55
Job time : 5.4947 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:21:06 ; Search time 19.3993 Seconds
(without alignments)
179.431 Million cell updates/sec

Title: US-10-684-957-43
Perfect score: 45
Sequence: 1 QRSGGSSFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	8	ADS87950	Ads87950 Anti-IFN-
2	45	100.0	9	8	ADS94947	Ads94947 Anti-IFN-
3	45	100.0	108	8	ADS87923	Ads87923 Anti-IFN-
4	45	100.0	108	8	ADS87915	Ads87915 Anti-IFN-
5	45	100.0	108	8	ADS87919	Ads87919 Anti-IFN-
6	45	100.0	108	8	ADS94920	Ads94920 Anti-IFN-
7	45	100.0	108	8	ADS94916	Ads94916 Anti-IFN-
8	45	100.0	108	8	ADS94912	Ads94912 Anti-IFN-
9	45	100.0	215	8	ADS87927	Ads87927 Anti-IFN-
10	45	100.0	215	8	ADS87929	Ads87929 Anti-IFN-
11	45	100.0	215	8	ADS87925	Ads87925 Anti-IFN-
12	45	100.0	215	8	ADS94926	Ads94926 Anti-IFN-
13	45	100.0	215	8	ADS94922	Ads94922 Anti-IFN-
14	45	100.0	215	8	ADS94924	Ads94924 Anti-IFN-
15	37	82.2	371	7	ADF59194	Adf59194 Human pol
16	37	82.2	1040	4	ABB65048	Abb65048 Drosophil
17	35	77.8	107	5	ABP33720	Abp33720 Human ORF
18	35	77.8	511	6	ADA48554	Ada48554 Rice prot
19	35	77.8	587	6	ABR52616	Abr52616 Protein s
20	35	77.8	587	7	ADK64144	Adk64144 Disease t
21	35	77.8	853	7	ABO64492	Abo64492 Klebsiell
22	34	75.6	22	4	ABG20272	Abg20272 Novel hum
23	34	75.6	115	2	AAY66179	Aay66179 Human bla
24	34	75.6	302	5	AAB71321	Aab71321 L. major
25	34	75.6	302	7	ADB78885	Adb78885 Leishmani
26	34	75.6	405	4	AAB30810	Aab30810 Amino aci
27	34	75.6	405	4	AAB30821	Aab30821 Amino aci
28	34	75.6	407	1	AAP94879	Aap94879 ORF incor
29	34	75.6	709	5	AAB71320	Aab71320 L. major
30	34	75.6	709	7	ADB78884	Adb78884 Leishmani
31	33	73.3	60	2	AAY00113	Aay00113 Enterococ
32	33	73.3	60	2	AAY00115	Aay00115 Enterococ
33	33	73.3	60	5	ABP43332	Abp43332 E faecali
34	33	73.3	60	5	ABP43334	Abp43334 E faecali
35	33	73.3	60	6	ABU88362	Abu88362 E. faecal
36	33	73.3	60	6	ABU88360	Abu88360 E. faecal
37	33	73.3	60	6	ABU13611	Abu13611 Enterococ
38	33	73.3	60	6	ABU13613	Abu13613 Enterococ
39	33	73.3	118	1	AAP80761	Aap80761 Deduced p
40	33	73.3	120	2	AAY00114	Aay00114 Enterococ
41	33	73.3	120	2	AAY00112	Aay00112 Enterococ
42	33	73.3	120	5	ABP43333	Abp43333 E faecali
43	33	73.3	120	5	ABP43331	Abp43331 E faecali
44	33	73.3	120	6	ABU88361	Abu88361 E. faecal
45	33	73.3	120	6	ABU88359	Abu88359 E. faecal

ALIGNMENTS

RESULT 1
ADS87950
ID ADS87950 standard; peptide; 9 AA.
XX
AC ADS87950;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain CDR3 SEQ ID NO:43.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87954.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 2; SEQ ID NO 43; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising

CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 1 QRSGGSSFT 9

RESULT 2
ADS94947
ID ADS94947 standard; peptide; 9 AA.
XX
AC ADS94947;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain CDR3 SEQ ID NO:43.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94951.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 2; SEQ ID NO 43; 115pp; English.

XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain complementarity determining region
CC (CDR), which is used in the exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 1 QRSGGSSFT 9

RESULT 3
ADS87923
ID ADS87923 standard; protein; 108 AA.
XX
AC ADS87923;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:16.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
DR N-PSDB; ADS87922.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or

```
PT   atherosclerosis.
XX
PS   Claim 9; SEQ ID NO 16; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 108 AA;

  Query Match             100.0%;  Score 45;  DB 8;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||||||
Db         90 QRSGGSSFT 98


RESULT 4
ADS87915
ID   ADS87915 standard; protein; 108 AA.
XX
AC   ADS87915;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody light chain variable region SEQ ID NO:8.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
DR   WPI; 2004-348323/32.
DR   N-PSDB; ADS87914.
XX
PT   New antibody that binds specifically to IFN-gamma and comprising a heavy
PT   chain CDR3, useful in preparing a composition for treating IFN-gamma
PT   mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT   atherosclerosis.
XX
PS   Claim 9; SEQ ID NO 8; 115pp; English.
XX
CC   The present invention describes an isolated antibody which binds
CC   specifically to interferon (IFN)-gamma and comprises a heavy chain
CC   complementarity determining region (CDR) 3 having a sequence comprising
CC   at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC   (ADS87943) in the same order and spacing, or an amino acid sequence of
CC   SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC   encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC   disease; and (3) a composition comprising a carrier and the antibody. The
CC   IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC   HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC   antidiabetic activities, and can be used in gene therapy. The antibody is
CC   useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC   arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC   disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC   nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC   Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC   or haemolytic anaemia. The present sequence represents an immunoglobulin
CC   G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 108 AA;

  Query Match             100.0%;  Score 45;  DB 8;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||||||
Db         90 QRSGGSSFT 98


RESULT 5
ADS87919
ID   ADS87919 standard; protein; 108 AA.
XX
AC   ADS87919;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti-IFN-gamma antibody light chain variable region SEQ ID NO:12.
XX
KW   antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW   anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW   antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW   gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW   multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW   myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW   systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW   vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW   immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2004034988-A2.
XX
PD   29-APR-2004.
XX
PF   14-OCT-2003; 2003WO-US032678.
XX
PR   16-OCT-2002; 2002US-0419057P.
PR   17-JUN-2003; 2003US-0479241P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Welcher A,  Chute H,  Li L,  Huang H;
XX
```

DR WPI; 2004-348323/32.
DR N-PSDB; ADS87918.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 9; SEQ ID NO 12; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 45; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 6
ADS94920
ID ADS94920 standard; protein; 108 AA.
XX
AC ADS94920;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:16.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94919.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 11; SEQ ID NO 16; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 45; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 7
ADS94916
ID ADS94916 standard; protein; 108 AA.
XX
AC ADS94916;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:12.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX

PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94915.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 11; SEQ ID NO 12; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 45; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 8
ADS94912
ID ADS94912 standard; protein; 108 AA.
XX
AC ADS94912;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody light chain variable region SEQ ID NO:8.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
DR N-PSDB; ADS94911.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 11; SEQ ID NO 8; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain variable region, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 45; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 9
ADS87927
ID ADS87927 standard; protein; 215 AA.
XX
AC ADS87927;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 or 1118* light chain SEQ ID NO:20.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX

OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 20; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

```
  Query Match             100.0%;  Score 45;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||||||
Db         90 QRSGGSSFT 98
```

RESULT 10
ADS87929
ID ADS87929 standard; protein; 215 AA.
XX
AC ADS87929;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 light chain SEQ ID NO:22.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 22; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

```
  Query Match             100.0%;  Score 45;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||||||
Db         90 QRSGGSSFT 98
```

RESULT 11
ADS87925
ID ADS87925 standard; protein; 215 AA.
XX
AC ADS87925;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 light chain SEQ ID NO:18.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;

KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004034988-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032678.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Welcher A, Chute H, Li L, Huang H;
XX
DR WPI; 2004-348323/32.
XX
PT New antibody that binds specifically to IFN-gamma and comprising a heavy
PT chain CDR3, useful in preparing a composition for treating IFN-gamma
PT mediated diseases e.g., AIDS, psoriasis, myasthenia gravis, cirrhosis or
PT atherosclerosis.
XX
PS Claim 15; SEQ ID NO 18; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS87943) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS87944). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 45; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 12
ADS94926
ID ADS94926 standard; protein; 215 AA.
XX
AC ADS94926;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1121 light chain SEQ ID NO:22.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 22; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 45; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 13
ADS94922
ID ADS94922 standard; protein; 215 AA.
XX
AC ADS94922;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1119 light chain SEQ ID NO:18.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;

KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 18; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 45; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 14
ADS94924
ID ADS94924 standard; protein; 215 AA.
XX
AC ADS94924;
XX
DT 02-DEC-2004 (first entry)
XX
DE Anti-IFN-gamma antibody 1118 or 1118* light chain SEQ ID NO:20.
XX
KW antibody; interferon gamma; IFN-gamma; IFN-gamma mediated disease;
KW anti-inflammatory; antiarthritic; anti-HIV; antianaemic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antidiabetic;
KW gene therapy; AIDS; rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis; Addison's disease; type I diabetes; psoriasis;
KW myasthenia gravis; cirrhosis; lupus nephritis; atherosclerosis;
KW systemic lupus erythematosus; sarcoidosis; Sjogren's syndrome;
KW vasculitis; Grave's disease; Guillain-Barre syndrome; haemolytic anaemia;
KW immunoglobulin G1; IgG1; anti-IFN-gamma antibody; human.
XX
OS Homo sapiens.
XX
PN WO2004035747-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US032871.
XX
PR 16-OCT-2002; 2002US-0419057P.
PR 17-JUN-2003; 2003US-0479241P.
XX
PA (AMGE-) AMGEN INC.
PA (MEDA-) MEDAREX INC.
XX
PI Welcher AA, Chute HT, Li Y, Huang H;
XX
DR WPI; 2004-348443/32.
XX
PT New human anti-interferon-gamma neutralizing antibodies for treating
PT interferon-gamma-mediated diseases, such as AIDS, rheumatoid arthritis,
PT diabetes, Grave's disease, psoriasis, atherosclerosis or transplant
PT rejection.
XX
PS Claim 17; SEQ ID NO 20; 115pp; English.
XX
CC The present invention describes an isolated antibody which binds
CC specifically to interferon (IFN)-gamma and comprises a heavy chain
CC complementarity determining region (CDR) 3 having a sequence comprising
CC at least 7 amino acids of the 8-amino acid sequence of SEQ ID NO:36
CC (ADS94940) in the same order and spacing, or an amino acid sequence of
CC SEQ ID NO:37 (ADS94941). Also described: (1) an isolated polynucleotide
CC encoding the antibody; (2) a method of treating an IFN-gamma mediated
CC disease; and (3) a composition comprising a carrier and the antibody. The
CC IFN-gamma binding antibody has anti-inflammatory, antiarthritic, anti-
CC HIV, antianaemic, antiarteriosclerotic, hepatotropic, antipsoriatic and
CC antidiabetic activities, and can be used in gene therapy. The antibody is
CC useful in treating IFN-gamma mediated disease, e.g., AIDS, rheumatoid
CC arthritis, inflammatory bowel disease, multiple sclerosis, Addison's
CC disease, type I diabetes, psoriasis, myasthenia gravis, cirrhosis, lupus
CC nephritis, atherosclerosis, systemic lupus erythematosus, sarcoidosis,
CC Sjogren's syndrome, vasculitis, Grave's disease, Guillain-Barre syndrome
CC or haemolytic anaemia. The present sequence represents an immunoglobulin
CC G1 (IgG1) anti-IFN-gamma light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 45; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 15
ADF59194
ID ADF59194 standard; protein; 371 AA.
XX
AC ADF59194;

XX
DT 12-FEB-2004 (first entry)
XX
DE Human polypeptide sequence SEQ ID NO:1602.
XX
KW biological activity; genetic engineering; hybridisation probe; oligomer;
KW primer; chromosome mapping; gene mapping; recombinant protein production;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003080795-A2.
XX
PD 02-OCT-2003.
XX
PF 09-AUG-2002; 2002WO-US025485.
XX
PR 09-AUG-2001; 2001US-0311261P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;
XX
DR WPI; 2003-876918/81.
DR N-PSDB; ADF58194.
XX
PT New polynucleotides, useful as hybridization probes, oligomers or
PT primers, for chromosome or gene mapping, for the recombinant production
PT of proteins, and for generating antisense DNA or RNA.
XX
PS Claim 20; SEQ ID NO 1602; 571pp; English.
XX
CC The present sequence represents a polypeptide (II) with biological
CC activity, which is encoded by an isolated polynucleotide sequence (I)
CC from the present invention . Also described: (1) a vector comprising (I);
CC (2) an expression vector comprising (I); (3) a host cell genetically
CC engineered to comprise (I) which is operatively associated with a
CC regulatory sequence that modulates expression of (I) in the host cell;
CC (4) a polypeptide (II) encoded by (I); (5) a composition comprising the
CC polypeptide of (4) and a carrier; (6) an antibody directed against the
CC polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a
CC sample; (8) identifying a compound that binds to the polypeptide of (4);
CC (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA.
XX
SQ Sequence 371 AA;

Query Match 82.2%; Score 37; DB 7; Length 371;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QRSGGSSFT 9
              |:||||||:
Db         47 QQSGGSSFS 55
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Search completed: August 18, 2005, 06:09:19
Job time : 21.3993 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:37:31 ; Search time 3.59364 Seconds
(without alignments)
240.968 Million cell updates/sec

Title: US-10-684-957-43
Perfect score: 45
Sequence: 1 QRSGGSSFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	35	77.8	569	2	T50414	probable prolifera
2	35	77.8	587	2	A56015	finger protein SIG
3	34	75.6	287	2	B86480	hypothetical prote
4	34	75.6	312	2	T47345	hypothetical prote
5	34	75.6	405	2	S19355	hypothetical prote
6	34	75.6	775	2	T48957	hypothetical prote
7	33	73.3	111	2	S41504	12RNP1 protein - S
8	33	73.3	196	2	T46326	hypothetical prote
9	33	73.3	251	2	T04866	hypothetical prote
10	33	73.3	311	2	G86324	hypothetical prote
11	33	73.3	552	2	T10186	glutamyl-tRNA redu
12	33	73.3	576	2	S75958	hypothetical prote
13	33	73.3	901	2	S65161	hypothetical prote
14	33	73.3	1099	2	AE1065	conserved hypothet
15	33	73.3	1168	1	MWAXIC	myosin heavy chain
16	33	73.3	1203	2	I55466	N-methyl-D-asparta
17	33	73.3	1239	2	I49705	glutamate receptor
18	33	73.3	1323	2	S27224	N-methyl-D-asparta
19	33	73.3	1323	2	I78557	N-methyl-D-asparta
20	33	73.3	1356	1	C45219	N-methyl-D-asparta
21	33	73.3	1723	2	H86557	polymorphic membra
22	33	73.3	1723	2	E72067	polymorphic membra
23	33	73.3	1732	2	C81601	polymorphic membra
24	32	71.1	187	2	E69170	hypothetical prote
25	32	71.1	329	2	T44459	arginine metabolis
26	32	71.1	412	2	AG3637	cis,cis-muconate t
27	32	71.1	447	2	T12978	hypothetical prote
28	32	71.1	452	2	T12981	hypothetical prote
29	32	71.1	798	2	T33022	hypothetical prote
30	32	71.1	1502	1	RGBYH1	CYC1/CYP3 transcri
31	32	71.1	2314	2	T28698	hypothetical prote
32	31	68.9	28	2	PQ0263	dnaK-type molecula
33	31	68.9	101	2	S71780	RNA-binding protei
34	31	68.9	207	2	E64718	conserved hypothet
35	31	68.9	209	2	T27459	hypothetical prote
36	31	68.9	209	2	A71800	hypothetical prote
37	31	68.9	255	2	T02010	expansin homolog T
38	31	68.9	272	2	AG0566	negative regulator
39	31	68.9	310	2	D71679	UDP-n-acetylenolpy
40	31	68.9	320	2	B97336	lactate dehydrogen
41	31	68.9	331	2	S57717	fructose-bisphosph
42	31	68.9	334	2	C84204	phosphate regulato
43	31	68.9	366	2	C81336	RodA protein homol
44	31	68.9	370	2	E96929	probable permease
45	31	68.9	378	2	D97741	hypothetical prote

ALIGNMENTS

RESULT 1
T50414
probable proliferation-associated serine/threonine protein kinase [imported] - fission y
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 16-Aug-2004
C;Accession: T50414
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25039
A;Accession: T50414
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-569 <SEE>
A;Cross-references: UNIPROT:Q9P7J8; EMBL:AL157991; PIDN:CAB76216.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h(-); cosmid c24B10
C;Genetics:
A;Gene: SPDB:SPCC24B10.07
A;Map position: 3
A;Introns: 8/1
C;Superfamily: protein kinase homology

Query Match 77.8%; Score 35; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 SGGSSFT 9
              |||||||
Db         22 SGGSSFT 28
```

RESULT 2
A56015
finger protein SIG1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YER068w; regulatory protein MOT2
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 09-Jul-2004
C;Accession: A56015; S46366; S47918; S50571
R;Irie, K.; Yamaguchi, K.; Kawase, K.; Matsumoto, K.
Mol. Cell. Biol. 14, 3150-3157, 1994
A;Title: The yeast MOT2 gene encodes a putative zinc finger protein that serves as a glo
ve genes.
A;Reference number: A56015; MUID:94217712; PMID:8164670
A;Accession: A56015
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-587 <IRI>
A;Cross-references: UNIPROT:P34909; GB:L26309; NID:g425481; PIDN:AAB00326.1; PID:g425482
R;Leberer, E.; Dignard, D.; Harcus, D.; Whiteway, M.; Thomas, D.Y.
EMBO J. 13, 3050-3064, 1994
A;Title: Molecular characterization of SIG1, a Saccharomyces cerevisiae gene involved in
A;Reference number: S46366; MUID:94313986; PMID:8039500
A;Accession: S46366

```
A;Molecule type: DNA
A;Residues: 1-587 <LEB>
A;Cross-references: EMBL:M96736; NID:g401814; PIDN:AAC37413.1; PID:g401815
R;Cade, R.M.; Errede, B.
Mol. Cell. Biol. 14, 3139-3149, 1994
A;Title: MOT2 encodes a negative regulator of gene expression that affects basal expres
A;Reference number: S47918; MUID:94217711; PMID:8164669
A;Accession: S47918
A;Molecule type: DNA
A;Residues: 1-587 <CAD>
A;Cross-references: EMBL:L26309; NID:g425481; PIDN:AAB00326.1; PID:g425482
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.
A;Reference number: S50557
A;Accession: S50571
A;Molecule type: DNA
A;Residues: 1-587 <DIE>
A;Cross-references: EMBL:U18813; NID:g1381127; PIDN:AAB64604.1; PID:g603304; MIPS:YER068
C;Genetics:
A;Gene: SGD:MOT2; SIG1
A;Cross-references: SGD:S0000870; MIPS:YER068w
A;Map position: 5R
C;Keywords: zinc finger

  Query Match             77.8%;  Score 35;  DB 2;  Length 587;
  Best Local Similarity   66.7%;  Pred. No. 49;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |:|||::||
Db        275 QQSGGTAFT 283


RESULT 3
B86480
hypothetical protein F10O5.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86480
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B86480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <STO>
A;Cross-references: UNIPROT:Q9C8C0; GB:AE005172; NID:g11055829; PIDN:AAG28298.1; GSPDB:G
C;Genetics:
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein F18P9.30

  Query Match             75.6%;  Score 34;  DB 2;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSS 7
              |||||||
Db        161 QRSGGSS 167


RESULT 4
T47345
hypothetical protein F18P9.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47345
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; M
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24458
A;Accession: T47345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <NYA>
A;Cross-references: UNIPROT:Q9M1L8; EMBL:AL138654
A;Experimental source: cultivar Columbia; BAC clone F18P9
C;Genetics:
A;Map position: 3
A;Introns: 22/2; 218/3; 247/1
A;Note: F18P9.30
C;Superfamily: Arabidopsis thaliana hypothetical protein F18P9.30

  Query Match             75.6%;  Score 34;  DB 2;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSS 7
              |||||||
Db         84 QRSGGSS 90


RESULT 5
S19355
hypothetical protein YCL028w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCL181
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S19355; S17471; C27061
R;Hollenberg, C.P.; Kleinhans, U.; Lutzenkirchen, K.; Ramezani Rad, M.; Xu, G.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19350
A;Accession: S19355
A;Molecule type: DNA
A;Residues: 1-405 <HOL>
A;Cross-references: UNIPROT:P25367; EMBL:X59720; NID:g1907116; PIDN:CAA42357.1; PID:e264
R;Ramezani Rad, M.; Luetzenkirchen, K.; Xu, G.; Kleinhans, U.; Hollenberg, C.P.
Yeast 7, 533-538, 1991
A;Title: The complete sequence of a 11,953 bp fragment from C1G on chromosome III encompa
A;Reference number: S17471; MUID:91377317; PMID:1897318
A;Accession: S17471
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-186 <RAM>
A;Cross-references: EMBL:S58084
R;Trueheart, J.; Boeke, J.D.; Fink, G.R.
Mol. Cell. Biol. 7, 2316-2328, 1987
A;Title: Two genes required for cell fusion during yeast conjugation: evidence for a phe
A;Reference number: A93093; MUID:87286864; PMID:3302672
A;Accession: C27061
A;Molecule type: DNA
A;Residues: 1-180,'T',182-322,'VHSQLWLPWQVPTWAITPIQIRVMGASNRLMSMVDRN','RMVNSNPMSTEDRNTAE
A;Cross-references: EMBL:M16717; NID:g171534; PIDN:AAA34615.1; PID:g171536
C;Genetics:
A;Gene: SGD:RNQ1
A;Cross-references: SGD:S0000533
A;Map position: 3L

  Query Match             75.6%;  Score 34;  DB 2;  Length 405;
  Best Local Similarity   87.5%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              | ||||||
Db        197 QSSGGSSF 204


RESULT 6
```

T48957
hypothetical protein T15B3.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T48957
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25009
A;Accession: T48957
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-775 <JOR>
A;Cross-references: UNIPROT:Q9LXV8; EMBL:AL163975; GSPDB:GN00061; ATSP:T15B3.170
A;Experimental source: cultivar Columbia; BAC clone T15B3
C;Genetics:
A;Gene: ATSP:T15B3.170
A;Map position: 3
A;Introns: 33/3; 135/3; 298/1; 376/2; 478/3; 551/3

Query Match 75.6%; Score 34; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSS 7
|||||||
Db 250 QRSGGSS 256

RESULT 7
S41504
12RNP1 protein - Synechococcus sp. (PCC 6301)
C;Species: Synechococcus sp.
A;Variety: PCC 6301
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: S41504
R;Sugita, M.; Sugiura, M.
Nucleic Acids Res. 22, 25-31, 1994
A;Title: The existence of eukaryotic ribonucleoprotein consensus sequence-type RNA-bindi
A;Reference number: S41504; MUID:94173658; PMID:7510387
A;Accession: S41504
A;Molecule type: DNA
A;Residues: 1-111 <SUG>
A;Experimental source: Synechococcus 6301
A;Note: the author did not translate the codon for residue 1
C;Superfamily: ribonucleoprotein repeat homology
F;2-69/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 73.3%; Score 33; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRSGGSSF 8
:|||| ||
Db 82 ERSGGGSF 89

RESULT 8
T46326
hypothetical protein DKFZp434B1113.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46326
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23037
A;Accession: T46326
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-196 <AAA>
A;Cross-references: UNIPROT:Q9NTI4; EMBL:AL137254
A;Experimental source: adult testis; clone DKFZp434B1113
C;Genetics:
A;Note: DKFZp434B1113.1

Query Match 73.3%; Score 33; DB 2; Length 196;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSF 8
:||||:||
Db 161 RRSGGASF 168

RESULT 9
T04866
hypothetical protein F28A21.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04866
R;Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15387
A;Accession: T04866
A;Molecule type: DNA
A;Residues: 1-251 <BEV>
A;Cross-references: UNIPROT:Q9SN40; EMBL:AL035526
A;Experimental source: cultivar Columbia; BAC clone F28A21
C;Genetics:
A;Map position: 4
A;Introns: 31/1; 155/1
A;Note: F28A21.150

Query Match 73.3%; Score 33; DB 2; Length 251;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
| ||||:|
Db 59 QEKGGSSYT 67

RESULT 10
G86324
hypothetical protein T29M8.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86324
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86324
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <STO>
A;Cross-references: UNIPROT:Q9LMB2; GB:AE005172; NID:g8954052; PIDN:AAF82225.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match 73.3%; Score 33; DB 2; Length 311;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSF 8
:|||||:|
Db 304 RRSGGSAF 311

RESULT 11

T10186
glutamyl-tRNA reductase (EC 1.2.1.-) - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10186
R;Tanaka, R.; Yoshida, K.; Nakayashiki, T.; Masuda, T.; Tsuji, H.; Inokuchi, H.; Tanaka,
Plant Physiol. 110, 1223-1230, 1996
A;Title: Differential expression of two hemA mRNAs encoding glutamyl-tRNA reductase prot
A;Reference number: Z16983; MUID:97088717; PMID:8934625
A;Accession: T10186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-552 <TAN>
A;Cross-references: UNIPROT:P93111; EMBL:D50407; NID:g1694925; PIDN:BAA08910.1; PID:g169
C;Genetics:
A;Gene: hemA
C;Function:
A;Description: catalyzes the reduction of glutamyl-tRNA(Glu) by NADPH to glutamic acid 1
A;Pathway: aminolevulinate biosynthesis; porphyrin biosynthesis
C;Superfamily: glutamyl-tRNA reductase
C;Keywords: aminolevulinate biosynthesis; NADP; oxidoreductase; porphyrin biosynthesis

  Query Match 73.3%; Score 33; DB 2; Length 552;
  Best Local Similarity 77.8%; Pred. No. 1.1e+02;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
||:| ||||
Db 49 QRTGVSSFT 57

RESULT 12
S75958
hypothetical protein slr0042 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75958
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75958
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-576 <KAN>
A;Cross-references: UNIPROT:Q59991; EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAA1080
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0042

  Query Match 73.3%; Score 33; DB 2; Length 576;
  Best Local Similarity 66.7%; Pred. No. 1.2e+02;
  Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
| :|||:||
Db 470 QANGGSAFT 478

RESULT 13
S65161
hypothetical protein YPL150w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P2597
C;Species: Saccharomyces cerevisiae
C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 16-Aug-2004
C;Accession: S65161; S69449
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65154
A;Accession: S65161
A;Molecule type: DNA
A;Residues: 1-901 <PUR>
A;Cross-references: UNIPROT:Q12152; EMBL:Z73506; NID:g1370319; PIDN:CAA97855.1; PID:e247
A;Experimental source: strain S288C (AB972)
R;Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies
ogue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant
A;Reference number: S69428
A;Accession: S69449
A;Molecule type: DNA
A;Residues: 1-901 <PUW>
A;Cross-references: EMBL:X96770; NID:g1403537; PIDN:CAA65571.1; PID:e239048; PID:g140355
C;Genetics:
A;Cross-references: SGD:S0006071
A;Map position: 16L
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;39-287/Domain: protein kinase homology <KIN>
F;47-55/Region: protein kinase ATP-binding motif

  Query Match 73.3%; Score 33; DB 2; Length 901;
  Best Local Similarity 75.0%; Pred. No. 1.9e+02;
  Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRSGGSSF 8
|||||: |
Db 305 QRSGGTQF 312

RESULT 14
AE1065
conserved hypothetical protein STY4851 [imported] - Salmonella enterica subsp. enterica s
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE1065
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE1065
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1099 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06970.1; PID:g16505611; GSPDB:GN00176
C;Genetics:
A;Gene: STY4851

  Query Match 73.3%; Score 33; DB 2; Length 1099;
  Best Local Similarity 75.0%; Pred. No. 2.3e+02;
  Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RSGGSSFT 9
: ||||||
Db 719 KGGGSSFT 726

RESULT 15
MWAXIC
myosin heavy chain IC - Acanthamoeba castellanii
N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Acanthamoeba castellanii
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: A33891; C34448; A24146
R;Jung, G.; Korn, E.D.; Hammer III, J.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 6720-6724, 1987
A;Title: The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like and non-myo
A;Reference number: A33891; MUID:88016163; PMID:3477803
A;Accession: A33891
A;Molecule type: DNA

A;Residues: 1-1168 <JUN>
A;Cross-references: UNIPROT:P10569; GB:J02974; NID:g155624; PIDN:AAA27707.1; PID:g155625
A;Note: this gene and protein are called MIB in this paper
R;Brzeska, H.; Lynch, T.J.; Martin, B.; Korn, E.D.
J. Biol. Chem. 264, 19340-19348, 1989
A;Title: The localization and sequence of the phosphorylation sites of Acanthamoeba myos
A;Reference number: A34448; MUID:90037074; PMID:2530230
A;Accession: C34448
A;Molecule type: protein
A;Residues: 308-314,'X',316-329 <BRZ>
C;Comment: In this protein, the coiled-coil rod-like region found in many myosin heavy c
he protein is globular and does not self-associate into filaments.
C;Genetics:
A;Gene: MIC
A;Introns: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 321/3; 371/3; 428/
C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolo
C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein; t
F;10-653/Domain: myosin motor domain homology <MMOT>
F;101-108/Region: nucleotide-binding motif A (P-loop)
F;543-564/Region: actin binding #status predicted
F;671-1168/Domain: carboxyl-terminal <CTD>
F;675-883/Region: basic
F;923-978/Region: alanine/glycine/proline-rich
F;983-1030/Domain: SH3 homology <SH3>
F;1034-1168/Region: alanine/glycine/proline-rich
F;107/Binding site: ATP (Lys) #status predicted
F;311/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 73.3%; Score 33; DB 1; Length 1168;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QRSGGSSFT 9
              : |||:|||
Db        903 ETSGGASFT 911
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Search completed: August 18, 2005, 06:20:13
Job time : 5.59364 secs

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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:22:31 ; Search time 16.8869 Seconds
(without alignments)
272.916 Million cell updates/sec

Title: US-10-684-957-43
Perfect score: 45
Sequence: 1 QRSGGSSFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	84.4	914	2	Q6F2J6	Q6f2j6 oryza sativ
2	37	82.2	1067	2	Q9VEV4	Q9vev4 drosophila
3	37	82.2	1103	2	Q7QCS1	Q7qcs1 anopheles g
4	36	80.0	625	2	Q82M18	Q82m18 streptomyce
5	35	77.8	249	2	Q6QFA9	Q6qfa9 triticum ae
6	35	77.8	464	1	SMA5_BRARE	Q9w7e7 brachydanio
7	35	77.8	464	2	Q7ZU01	Q7zu01 brachydanio
8	35	77.8	569	1	GAD8_SCHPO	Q9p7j8 schizosacch
9	35	77.8	587	1	NOT4_YEAST	P34909 saccharomyc
10	35	77.8	597	2	Q6H6H0	Q6h6h0 oryza sativ
11	35	77.8	616	2	Q949C2	Q949c2 oryza sativ
12	35	77.8	771	2	Q8CDV5	Q8cdv5 mus musculu
13	35	77.8	795	2	O62006	O62006 branchiosto
14	35	77.8	875	2	Q7EZV4	Q7ezv4 oryza sativ
15	35	77.8	1044	2	Q9LG78	Q9lg78 oryza sativ
16	34	75.6	135	2	Q9CTV6	Q9ctv6 mus musculu
17	34	75.6	251	2	Q6QFA8	Q6qfa8 triticum ae
18	34	75.6	255	2	Q9FW90	Q9fw90 oryza sativ
19	34	75.6	287	2	Q9C8C0	Q9c8c0 arabidopsis
20	34	75.6	312	2	Q9M1L8	Q9m1l8 arabidopsis
21	34	75.6	405	1	RNQ1_YEAST	P25367 saccharomyc
22	34	75.6	473	2	Q6NZP2	Q6nzp2 mus musculu
23	34	75.6	473	2	Q8BI03	Q8bi03 mus musculu
24	34	75.6	473	2	Q8K2H8	Q8k2h8 mus musculu
25	34	75.6	475	2	Q8BHW7	Q8bhw7 mus musculu
26	34	75.6	629	2	Q7RX85	Q7rx85 neurospora
27	34	75.6	709	2	Q9XZX9	Q9xzx9 leishmania
28	34	75.6	775	2	Q9LXV8	Q9lxv8 arabidopsis
29	34	75.6	827	2	Q6G2D4	Q6g2d4 bartonella
30	34	75.6	1049	2	Q6C3Z3	Q6c3z3 yarrowia li
31	34	75.6	1384	2	Q8X0V2	Q8x0v2 neurospora
32	33	73.3	75	2	Q6YXS3	Q6yxs3 oryza sativ
33	33	73.3	107	2	Q53321	Q53321 synechococc
34	33	73.3	107	2	Q55345	Q55345 synechococc
35	33	73.3	107	2	Q79F26	Q79f26 synechococc
36	33	73.3	120	2	Q82Z26	Q82z26 enterococcu
37	33	73.3	120	2	Q82ZI0	Q82zi0 enterococcu
38	33	73.3	196	2	Q9NTI4	Q9nti4 homo sapien
39	33	73.3	225	2	Q8AWW4	Q8aww4 xenopus lae
40	33	73.3	251	2	Q9SN40	Q9sn40 arabidopsis
41	33	73.3	264	2	Q7PY71	Q7py71 anopheles g
42	33	73.3	265	2	Q75KB6	Q75kb6 oryza sativ
43	33	73.3	268	2	Q9VXV7	Q9vxv7 drosophila
44	33	73.3	308	2	Q8EHR6	Q8ehr6 shewanella
45	33	73.3	311	2	Q8LAP2	Q8lap2 arabidopsis

ALIGNMENTS

RESULT 1
Q6F2J6
ID Q6F2J6 PRELIMINARY; PRT; 914 AA.
AC Q6F2J6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative SWI/SNF complex protein.
GN Name=B1154F06.22;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 Myb-like domain.
DR EMBL; AC146936; AAT76383.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR007526; SWIRM.
DR InterPro; IPR000433; Znf_ZZ.
DR Pfam; PF00249; Myb_DNA-binding; 1.
DR Pfam; PF04433; SWIRM; 1.
DR Pfam; PF00569; ZZ; 1.
DR SMART; SM00717; SANT; 1.
DR SMART; SM00291; ZnF_ZZ; 1.
DR PROSITE; PS50090; MYB_3; 1.
DR PROSITE; PS50934; SWIRM; 1.
DR PROSITE; PS01357; ZF_ZZ_1; UNKNOWN_1.
DR PROSITE; PS50135; ZF_ZZ_2; 1.
KW Nuclear protein.
SQ SEQUENCE 914 AA; 98722 MW; 7D3C29892FD70661 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 914;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9

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              ::|||||||
Db          30 RKSGGSSFT 38


RESULT 2
Q9VEV4
ID   Q9VEV4       PRELIMINARY;      PRT;  1067 AA.
AC   Q9VEV4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CG12753-PA.
GN   ORFNames=CG12753;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003713; AAF55313.2; -.
DR   FlyBase; FBgn0038427; CG12753.
DR   InterPro; IPR011028; Cyclin_like.
SQ   SEQUENCE   1067 AA;  119366 MW;  E325AA430AA57394 CRC64;

  Query Match             82.2%;  Score 37;  DB 2;  Length 1067;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              |:||||||
Db         86 QKSGGSSF 93


RESULT 3
Q7QCS1
ID   Q7QCS1       PRELIMINARY;      PRT;  1103 AA.
AC   Q7QCS1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP1771 (Fragment).
GN   Name=agCG46066; ORFNames=ENSANGG00000019596;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008859; EAA07864.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   1103 AA;  122729 MW;  6308EC9B0AD6E14E CRC64;

  Query Match             82.2%;  Score 37;  DB 2;  Length 1103;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              |:||||||
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Db        105 QKSGGSSF 112


RESULT 4
Q82M18
ID   Q82M18      PRELIMINARY;      PRT;   625 AA.
AC   Q82M18;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative neuraminidase.
GN   Name=nanH; OrderedLocusNames=SAV1842;
OS   Streptomyces avermitilis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=33903;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MA-4680;
RX   MEDLINE=22608306; PubMed=12692562;
RA   Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA   Sakaki Y., Hattori M., Omura S.;
RT   "Complete genome sequence and comparative analysis of the industrial
RT   microorganism Streptomyces avermitilis.";
RL   Nat. Biotechnol. 21:526-531(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA   Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA   Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA   Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT   "Genome sequence of an industrial microorganism Streptomyces
RT   avermitilis: deducing the ability of producing secondary
RT   metabolites.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR   EMBL; AP005028; BAC69553.1; -.
DR   HSSP; Q02834; 1EUS.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR002860; Glyco_hydro_BNR.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR011040; Sialidase.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF02012; BNR; 5.
DR   Pfam; PF02210; Laminin_G_2; 1.
DR   SMART; SM00282; LamG; 1.
KW   Complete proteome.
SQ   SEQUENCE   625 AA;  67137 MW;  CAD6DA2F546FEAD7 CRC64;

  Query Match             80.0%;  Score 36;  DB 2;  Length 625;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 RSGGSSFT 9
              | ||||||
Db        288 RDGGSSFT 295


RESULT 5
Q6QFA9
ID   Q6QFA9      PRELIMINARY;      PRT;   249 AA.
AC   Q6QFA9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Expansin EXPA4.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhan L., Zhong F.N., Qi X.S.;
RT   "Isolation and characterization of novel expansins in wheat.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the expansin family.
DR   EMBL; AY543530; AAS48873.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR   InterPro; IPR009009; Barwin_like.
DR   InterPro; IPR002963; Expansin.
DR   InterPro; IPR007112; Expan_endogl.
DR   InterPro; IPR007118; Expan_Lol_pI.
DR   InterPro; IPR007117; Expan_Lol_pI_C.
DR   InterPro; IPR005132; Lipoprotein_13.
DR   Pfam; PF03330; DPBB_1; 1.
DR   Pfam; PF01357; Pollen_allerg_1; 1.
DR   PRINTS; PR01226; EXPANSIN.
DR   PRINTS; PR01225; EXPANSNFAMLY.
DR   ProDom; PD002179; Expan_Lol_pI_C; 1.
DR   PROSITE; PS50843; EXPANSIN_CBD; 1.
DR   PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ   SEQUENCE   249 AA;  27136 MW;  9E60AA78E04EB3C4 CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 249;
  Best Local Similarity   77.8%;  Pred. No. 91;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||  ||
Db        152 QRSGGMRFT 160


RESULT 6
SMA5_BRARE
ID   SMA5_BRARE     STANDARD;      PRT;   464 AA.
AC   Q9W7E7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mothers against decapentaplegic homolog 5 (SMAD 5) (Mothers against
DE   DPP homolog 5) (Smad5) (Somitabun protein).
GN   Name=smad5; Synonyms=madh5, sbn;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A., VARIANT ILE-429, FUNCTION, AND DEVELOPMENTAL
RP   STAGE.
RC   TISSUE=Gastrula;
RX   MEDLINE=99225462; PubMed=10207140;
RA   Hild M., Dick A., Rauch G.J., Meier A., Bouwmeester T., Haffter P.,
RA   Hammerschmidt M.;
RT   "The smad5 mutation somitabun blocks Bmp2b signaling during early
RT   dorsoventral patterning of the zebrafish embryo.";
RL   Development 126:2149-2159(1999).
RN   [2]
RP   SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC   TISSUE=Gastrula;
RX   MEDLINE=99454756; PubMed=10525190; DOI=10.1016/S0925-4773(99)00173-2;
RA   Mueller F., Blader P., Rastegar S., Fischer N., Knoechel W.,
RA   Straehle U.;
RT   "Characterization of zebrafish smad1, smad2 and smad5: the amino-
RT   terminus of Smad1 and Smad5 is required for specific function in the
RT   embryo.";
RL   Mech. Dev. 88:73-88(1999).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20058452; PubMed=10590480;
RX   DOI=10.1002/(SICI)1097-0177(199911)216:3<285::AID-DVDY7>3.0.CO;2-L;
RA   Dick A., Meier A., Hammerschmidt M.;
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RT   "Smad1 and smad5 have distinct roles during dorsoventral patterning of
RT   the zebrafish embryo.";
RL   Dev. Dyn. 216:285-298(1999).
CC   -!- FUNCTION: Involved in ventralization. May mediate Bmp2b signaling
CC       during early phases of embryonic dorsal-ventral pattern formation.
CC       Required for initation of Smad1 expression during gastrulation.
CC   -!- SUBUNIT: May form trimers with the co-SMAD SMAD4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: In the cytoplasm in the absence of ligand;
CC       migration to the nucleus when complexed with SMAD4 (By
CC       similarity).
CC   -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC       Uniform distribution at the cleavage, blastula, gastrula and early
CC       somitogenesis stages. Levels decline during the early gastrula
CC       stages. At 26 hours, still expressed in the head, forming gut and
CC       dorsal neural tube.
CC   -!- SIMILARITY: Belongs to the dwarfin/SMAD family.
CC   -!- SIMILARITY: Contains 1 DWA/MH1 domain.
CC   -!- SIMILARITY: Contains 1 DWB/MH2 domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF127920; AAD43904.1; -.
DR   EMBL; AF168775; AAF06738.1; -.
DR   HSSP; Q15797; 1KHU.
DR   TRANSFAC; T04152; -.
DR   ZFIN; ZDB-GENE-990603-9; smad5.
DR   GO; GO:0005737; C:cytoplasm; ISS.
DR   GO; GO:0005634; C:nucleus; ISS.
DR   GO; GO:0003700; F:transcription factor activity; NAS.
DR   GO; GO:0030509; P:BMP signaling pathway; IMP.
DR   GO; GO:0009880; P:embryonic pattern specification; IMP.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR   InterPro; IPR001132; Dwarfin.
DR   InterPro; IPR003619; Dwarfin_A.
DR   InterPro; IPR008984; SMAD_FHA.
DR   Pfam; PF03165; MH1; 1.
DR   Pfam; PF03166; MH2; 1.
DR   SMART; SM00523; DWA; 1.
DR   SMART; SM00524; DWB; 1.
KW   Developmental protein; Multigene family; Polymorphism;
KW   Transcription regulation.
FT   DOMAIN       26    135       DWA.
FT   DOMAIN      187    231       Pro-rich.
FT   DOMAIN      268    440       DWB.
FT   DOMAIN       40     46       Poly-Lys.
FT   VARIANT     429    429       T -> I (in allele DTC24; dorsalized
FT                                embryos).
SQ   SEQUENCE   464 AA;  51860 MW;  5018387FBA4072DC CRC64;

  Query Match             77.8%;  Score 35;  DB 1;  Length 464;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              | ||||||
Db        179 QHSGGSSF 186


RESULT 7
Q7ZU01
ID   Q7ZU01      PRELIMINARY;      PRT;   464 AA.
AC   Q7ZU01;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MAD homolog 5.
GN   Name=smad5;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB; TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB; TISSUE=Whole body;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC050481; AAH50481.1; -.
DR   HSSP; Q15797; 1KHU.
DR   ZFIN; ZDB-GENE-990603-9; smad5.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001132; Dwarfin.
DR   InterPro; IPR003619; Dwarfin_A.
DR   InterPro; IPR008984; SMAD_FHA.
DR   Pfam; PF03165; MH1; 1.
DR   Pfam; PF03166; MH2; 1.
DR   SMART; SM00523; DWA; 1.
DR   SMART; SM00524; DWB; 1.
SQ   SEQUENCE   464 AA;  51920 MW;  FA7171A1DF648C2E CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 464;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              | ||||||
Db        179 QHSGGSSF 186


RESULT 8
GAD8_SCHPO
ID   GAD8_SCHPO      STANDARD;      PRT;   569 AA.
AC   Q9P7J8;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Serine/threonine-protein kinase gad8 (EC 2.7.1.37).
GN   Name=gad8; ORFNames=SPCC24B10.07;
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
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```
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
RN   [2]
RP   FUNCTION, PHOSPHORYLATION OF TYR-387; SER-527 AND SER-546, AND
RP   MUTAGENESIS OF THR-387; SER-527 AND SER-546.
RX   PubMed=12805221; DOI=10.1093/emboj/cdg298;
RA   Matsuo T., Kubo Y., Watanabe Y., Yamamoto M.;
RT   "Schizosaccharomyces pombe AGC family kinase Gad8p forms a conserved
RT   signaling module with TOR and PDK1-like kinases.";
RL   EMBO J. 22:3073-3083(2003).
CC   -!- FUNCTION: Involved in a signaling module for sexual development
CC       and cell growth under stressed conditions. Required for G1 arrest
CC       under nitrogen starvation and for growth at high temperature and
CC       osmolarity.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Phosphorylated by ksg1 and tor1.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. AGC
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL157991; CAB76216.1; -.
DR   PIR; T50414; T50414.
DR   HSSP; P31751; 1GZK.
DR   GeneDB_SPombe; SPCC24B10.07; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN      168    173       Poly-Ser.
FT   DOMAIN      230    485       Protein kinase.
FT   NP_BIND     236    244       ATP (By similarity).
FT   BINDING     259    259       ATP (By similarity).
FT   ACT_SITE    353    353       Proton acceptor (By similarity).
FT   MOD_RES     387    387       Phosphothreonine.
FT   MOD_RES     527    527       Phosphoserine (by PI3K).
FT   MOD_RES     546    546       Phosphoserine (by PI3K).
FT   MUTAGEN     387    387       T->A: Sterile and no growth under
FT                                stressed conditions.
FT   MUTAGEN     387    387       T->D,E: No activity.
FT   MUTAGEN     527    527       S->A: Sterile and no growth under
FT                                stressed conditions.
FT   MUTAGEN     527    527       S->D: Function compromised.
FT   MUTAGEN     546    546       S->A: Fertile and no growth defects.
FT   MUTAGEN     546    546       S->D: Function compromised.
SQ   SEQUENCE   569 AA;  63769 MW;  B2A510D5266D0BE8 CRC64;

  Query Match             77.8%;  Score 35;  DB 1;  Length 569;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SGGSSFT 9
              |||||||
Db         22 SGGSSFT 28


RESULT 9
NOT4_YEAST
ID   NOT4_YEAST     STANDARD;      PRT;   587 AA.
AC   P34909;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   General negative regulator of transcription subunit 4.
GN   Name=NOT4; Synonyms=CCL1, MOT2, SIG1, SSF1; OrderedLocusNames=YER068W;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94313986; PubMed=8039500;
RA   Leberer E., Dignard D., Harcus D., Whiteway M., Thomas D.Y.;
RT   "Molecular characterization of SIG1, a Saccharomyces cerevisiae gene
RT   involved in negative regulation of G-protein-mediated signal
RT   transduction.";
RL   EMBO J. 13:3050-3064(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94217711; PubMed=8164669;
RA   Cade R.M., Errede B.;
RT   "MOT2 encodes a negative regulator of gene expression that affects
RT   basal expression of pheromone-responsive genes in Saccharomyces
RT   cerevisiae.";
RL   Mol. Cell. Biol. 14:3139-3149(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94217712; PubMed=8164670;
RA   Irie K., Yamaguchi K., Kawase K., Matsumoto K.;
RT   "The yeast MOT2 gene encodes a putative zinc finger protein that
RT   serves as a global negative regulator affecting expression of several
RT   categories of genes, including mating-pheromone-responsive genes.";
RL   Mol. Cell. Biol. 14:3150-3157(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=97313264; PubMed=9169868;
RA   Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA   Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA   Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
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RA   Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA   Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA   Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA   Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL   Nature 387:78-81(1997).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=95011559; PubMed=7926748;
RA   Collart M.A., Struhl K.;
RT   "NOT1(CDC39), NOT2(CDC36), NOT3, and NOT4 encode a global-negative
RT   regulator of transcription that differentially affects TATA-element
RT   utilization.";
RL   Genes Dev. 8:525-537(1994).
CC   -!- FUNCTION: Negatively regulates the basal and activated
CC       transcription of many genes. Preferentially affects non-consencsus
CC       (TC-type) TATA element-dependent transcription. Could directly or
CC       indirectly inhibits component(s) of the general transcription
CC       machinery.
CC   -!- SUBUNIT: Forms a complex that comprise NOT1, NOT2, NOT3, NOT4 and
CC       NOT5.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M96736; AAC37413.1; -.
DR   EMBL; L26309; AAB00326.1; -.
DR   EMBL; U18813; AAB64604.1; -.
DR   PIR; A56015; A56015.
DR   HSSP; O95628; 1E4U.
DR   GermOnline; 139148; -.
DR   TRANSFAC; T03591; -.
DR   SGD; S000000870; MOT2.
DR   GO; GO:0030015; C:CCR4-NOT core complex; IPI.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0000175; F:3'-5'-exoribonuclease activity; IDA.
DR   GO; GO:0000747; P:conjugation with cellular fusion; IMP.
DR   GO; GO:0000289; P:poly(A) tail shortening; IDA.
DR   GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IPI.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00076; RRM_1; 1.
DR   PROSITE; PS50102; RRM; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Coiled coil; Nuclear protein; Repressor; RNA-binding;
KW   Transcription regulation; Zinc-finger.
FT   ZN_FING      33     78       RING-type.
FT   DOMAIN       94    128       Coiled coil (Potential).
FT   DOMAIN      137    232       RNA-binding (RRM).
SQ   SEQUENCE   587 AA;  65354 MW;  8847084BD9BF48B7 CRC64;

  Query Match             77.8%;  Score 35;  DB 1;  Length 587;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |:|||::||
Db        275 QQSGGTAFT 283


RESULT 10
Q6H6H0
ID   Q6H6H0      PRELIMINARY;      PRT;   597 AA.
AC   Q6H6H0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative cell division cycle protein 23.
GN   Name=P0519E06.25;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
RT   clone:P0519E06.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP005006; BAD25679.1; -.
DR   GO; GO:0005680; C:anaphase-promoting complex; IEA.
DR   GO; GO:0000910; P:cytokinesis; IEA.
DR   GO; GO:0030071; P:regulation of mitotic metaphase/anaphase tr. . .; IEA.
DR   InterPro; IPR007192; APC8.
DR   InterPro; IPR008940; Prenyl_trans.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF04049; APC8; 1.
DR   Pfam; PF00515; TPR_1; 6.
DR   SMART; SM00028; TPR; 7.
DR   PROSITE; PS50005; TPR; 2.
DR   PROSITE; PS50293; TPR_REGION; 1.
KW   Cell division; Repeat; TPR repeat.
SQ   SEQUENCE   597 AA;  68065 MW;  E1ED26D0F83478CB CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 597;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RSGGSSF 8
              |||||||
Db         70 RSGGSSF 76


RESULT 11
Q949C2
ID   Q949C2      PRELIMINARY;      PRT;   616 AA.
AC   Q949C2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anaphase-promoting complex subunit 8-like protein.
GN   Name=W920ERIPDK;
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R;
RA   Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,
RA   Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K.,
RA   Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,
RA   Bevan M., Bancroft I.;
RT   "Conservation of microstructure bewtween a sequenced region of the
RT   genome of rice and multiple segments of the genome of Arabidopsis
RT   thaliana.";
RL   Genome Res. 11:1167-1174(2001).
DR   EMBL; AJ307662; CAC39070.1; -.
DR   Gramene; Q949C2; -.
DR   GO; GO:0005680; C:anaphase-promoting complex; IEA.
DR   GO; GO:0030071; P:regulation of mitotic metaphase/anaphase tr. . .; IEA.
DR   InterPro; IPR007192; APC8.
DR   InterPro; IPR008940; Prenyl_trans.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF04049; APC8; 1.
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DR   Pfam; PF00515; TPR_1; 4.
DR   SMART; SM00028; TPR; 6.
DR   PROSITE; PS50005; TPR; 2.
DR   PROSITE; PS50293; TPR_REGION; 1.
KW   Repeat; TPR repeat.
SQ   SEQUENCE   616 AA;  70104 MW;  9D0FC37E547EC39B CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 616;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RSGGSSF 8
              |||||||
Db         70 RSGGSSF 76


RESULT 12
Q8CDV5
ID   Q8CDV5      PRELIMINARY;      PRT;   771 AA.
AC   Q8CDV5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE   library, clone:4921511K13 product:a disintegrin and metalloprotease
DE   domain 5, full insert sequence.
GN   Name=Adam5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK029519; BAC26490.1; -.
DR   HSSP; P21859; 1J2L.
DR   MEROPS; M12.953; -.
DR   MGD; MGI:104730; Adam5.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR006586; ADAM_cysteine.
DR   InterPro; IPR001762; Disintegrin.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001590; Peptidase_M12B.
DR   InterPro; IPR002870; Peptidase_M12B_N.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   Pfam; PF00200; Disintegrin; 1.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF01562; Pep_M12B_propep; 1.
DR   Pfam; PF01421; Reprolysin; 1.
DR   ProDom; PD000664; Disintegrin; 1.
DR   SMART; SM00608; ACR; 1.
DR   SMART; SM00050; DISIN; 1.
DR   PROSITE; PS50215; ADAM_MEPRO; 1.
DR   PROSITE; PS50214; DISINTEGRIN_2; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW   Integrin; Metalloprotease; Protease.
SQ   SEQUENCE   771 AA;  86874 MW;  E2D4FF67003006CD CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 771;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SGGSSFT 9
              |||||||
Db        745 SGGSSFT 751


RESULT 13
O62006
ID   O62006      PRELIMINARY;      PRT;   795 AA.
AC   O62006;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Intermediate filament protein C2.
OS   Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7740;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole animal;
RX   MEDLINE=98267218; PubMed=9602172; DOI=10.1016/S0378-1119(98)00151-6;
RA   Riemer D., Karabinos A., Weber K.;
RT   "Analysis of eight cDNAs and six genes for intermediate filament (IF)
RT   proteins in the cephalochordate Branchiostoma reveals differences in
```

```
RT   the IF multigene families of lower chordates and the vertebrates.";
RL   Gene 211:361-373(1998).
CC   -!- SIMILARITY: Belongs to the intermediate filament family.
DR   EMBL; AJ223578; CAA11445.1; -.
DR   HSSP; P08670; 1GK7.
DR   GO; GO:0005882; C:intermediate filament; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR011000; ApoLp_III_like.
DR   InterPro; IPR001664; IF.
DR   InterPro; IPR002957; Keratin_I.
DR   Pfam; PF00038; Filament; 1.
DR   PRINTS; PR01248; TYPE1KERATIN.
DR   PROSITE; PS00226; IF; UNKNOWN_1.
KW   Intermediate filament.
SQ   SEQUENCE   795 AA;  84532 MW;  D00B2665CEAC7FFC CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RSGGSSF 8
              |||||||
Db         31 RSGGSSF 37


RESULT 14
Q7EZV4
ID   Q7EZV4      PRELIMINARY;      PRT;   875 AA.
AC   Q7EZV4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative dynamin homolog.
GN   Name=P0456B03.108;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the dynamin family.
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AP004463; BAC98559.2; -.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   InterPro; IPR002464; DEAH_box.
DR   InterPro; IPR001401; Dynamin.
DR   InterPro; IPR000375; Dynamin_central.
DR   InterPro; IPR003130; GED.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011036; PH_related.
DR   Pfam; PF01031; Dynamin_M; 1.
DR   Pfam; PF00350; Dynamin_N; 1.
DR   Pfam; PF02212; GED; 1.
DR   Pfam; PF00169; PH; 1.
DR   PRINTS; PR00195; DYNAMIN.
DR   SMART; SM00053; DYNc; 1.
DR   SMART; SM00233; PH; 1.
DR   PROSITE; PS00690; DEAH_ATP_HELICASE; UNKNOWN_1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   GTP-binding.
SQ   SEQUENCE   875 AA;  95552 MW;  32577438250EA95F CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 875;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              || |||||
Db         32 QRRGGSSF 39


RESULT 15
Q9LG78
ID   Q9LG78      PRELIMINARY;      PRT;  1044 AA.
AC   Q9LG78;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   P0710E05.19 protein.
GN   Name=P0710E05.19;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=12447438; DOI=10.1038/nature01184;
RA   Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA   Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA   Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA   Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA   Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA   Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA   Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA   Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA   Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA   Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA   Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA   Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA   Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA   Yano M., Jiang J., Gojobori T.;
RT   "The genome sequence and structure of rice chromosome 1.";
RL   Nature 420:312-316(2002).
DR   EMBL; AP002743; BAA99432.3; -.
DR   Gramene; Q9LG78; -.
DR   InterPro; IPR011038; Calycin.
DR   InterPro; IPR007228; DUF390.
DR   InterPro; IPR007321; Transposase_28.
DR   Pfam; PF04094; DUF390; 2.
DR   Pfam; PF04195; Transposase_28; 1.
SQ   SEQUENCE   1044 AA;  112949 MW;  607AD5C771E0483B CRC64;

  Query Match             77.8%;  Score 35;  DB 2;  Length 1044;
  Best Local Similarity   77.8%;  Pred. No. 4.2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              ||||| | |
Db        444 QRSGGESLT 452


Search completed: August 18, 2005, 06:18:21
Job time : 18.8869 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 05:39:37 ; Search time 5.05654 Seconds
(without alignments)
132.866 Million cell updates/sec

Title: US-10-684-957-43
Perfect score: 45
Sequence: 1 QRSGGSSFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	35	77.8	853	4	US-09-489-039A-11009	Sequence 11009, A
2	34	75.6	302	4	US-09-874-923-122	Sequence 122, App
3	34	75.6	709	4	US-09-874-923-121	Sequence 121, App
4	33	73.3	60	4	US-09-071-035-208	Sequence 208, App
5	33	73.3	60	4	US-09-071-035-212	Sequence 212, App
6	33	73.3	120	4	US-09-071-035-206	Sequence 206, App
7	33	73.3	120	4	US-09-071-035-210	Sequence 210, App
8	33	73.3	143	4	US-09-134-000C-6044	Sequence 6044, Ap
9	33	73.3	407	4	US-09-489-039A-11488	Sequence 11488, A
10	33	73.3	609	4	US-09-198-452A-579	Sequence 579, App
11	33	73.3	1025	4	US-09-543-681A-7112	Sequence 7112, Ap
12	33	73.3	1239	1	US-08-026-138E-3	Sequence 3, Appli
13	33	73.3	1323	1	US-08-026-138E-4	Sequence 4, Appli
14	33	73.3	1336	2	US-08-231-193A-58	Sequence 58, Appl
15	33	73.3	1336	2	US-08-486-273A-58	Sequence 58, Appl
16	33	73.3	1336	3	US-08-940-086A-58	Sequence 58, Appl
17	33	73.3	1336	3	US-08-940-035A-58	Sequence 58, Appl
18	33	73.3	1336	3	US-08-935-105A-58	Sequence 58, Appl
19	33	73.3	1336	4	US-09-648-797-58	Sequence 58, Appl
20	33	73.3	1336	4	US-09-386-123-58	Sequence 58, Appl
21	33	73.3	1336	4	US-10-038-937-58	Sequence 58, Appl
22	33	73.3	1345	4	US-09-949-016-11209	Sequence 11209, A
23	33	73.3	1368	4	US-09-967-908A-2	Sequence 2, Appli
24	33	73.3	1368	4	US-10-159-151-2	Sequence 2, Appli
25	33	73.3	1744	4	US-09-438-185A-542	Sequence 542, App
26	32	71.1	63	4	US-09-621-976-4372	Sequence 4372, Ap
27	32	71.1	226	3	US-08-651-136C-16	Sequence 16, Appl
28	32	71.1	226	3	US-09-229-911A-16	Sequence 16, Appl
29	32	71.1	293	3	US-08-651-136C-20	Sequence 20, Appl
30	32	71.1	293	3	US-09-229-911A-20	Sequence 20, Appl
31	32	71.1	298	3	US-08-651-136C-18	Sequence 18, Appl
32	32	71.1	298	3	US-09-229-911A-18	Sequence 18, Appl
33	32	71.1	306	4	US-09-902-540-11146	Sequence 11146, A
34	32	71.1	332	4	US-09-252-991A-29873	Sequence 29873, A
35	32	71.1	387	4	US-09-949-016-7720	Sequence 7720, Ap
36	32	71.1	435	4	US-09-248-796A-15070	Sequence 15070, A
37	31	68.9	38	3	US-08-706-344C-7	Sequence 7, Appli
38	31	68.9	192	3	US-09-397-992A-24	Sequence 24, Appl
39	31	68.9	192	4	US-09-971-843-24	Sequence 24, Appl
40	31	68.9	214	4	US-09-252-991A-31981	Sequence 31981, A
41	31	68.9	310	3	US-09-632-947B-8	Sequence 8, Appli
42	31	68.9	397	4	US-09-248-796A-14210	Sequence 14210, A
43	31	68.9	447	4	US-09-252-991A-20563	Sequence 20563, A
44	31	68.9	513	4	US-09-248-796A-25078	Sequence 25078, A
45	31	68.9	519	4	US-09-252-991A-26230	Sequence 26230, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11009
; Sequence 11009, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11009
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11009

Query Match 77.8%; Score 35; DB 4; Length 853;
Best Local Similarity 77.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 QRSGGSSFT 9
              || || |||
Db        163 QRQGGVSFT 171
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RESULT 2
US-09-874-923-122
; Sequence 122, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 122
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Leishmania major and chagasi
US-09-874-923-122

  Query Match             75.6%;  Score 34;  DB 4;  Length 302;
  Best Local Similarity   77.8%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |  ||||||
Db         10 QEIGGSSFT 18


RESULT 3
US-09-874-923-121
; Sequence 121, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
;  APPLICANT: Reed, Steven G.
;  APPLICANT:  Campos-Neto, Antonio
;  APPLICANT:  Webb, John R.
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Coler, Rhea
;  APPLICANT:  Probst, Peter
;  APPLICANT:  Brannon, Mark
;  TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF LEISHMANIASIS
;  FILE REFERENCE: 210121.420C8
;  CURRENT APPLICATION NUMBER: US/09/874,923
;  CURRENT FILING DATE:  2001-06-04
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 121
;   LENGTH: 709
;   TYPE: PRT
;   ORGANISM: Leishmania major and chagasi
US-09-874-923-121

  Query Match             75.6%;  Score 34;  DB 4;  Length 709;
  Best Local Similarity   77.8%;  Pred. No. 4.4e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |  ||||||
Db         32 QEIGGSSFT 40


RESULT 4
US-09-071-035-208
; Sequence 208, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  208:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  60 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-208

  Query Match             73.3%;  Score 33;  DB 4;  Length 60;
  Best Local Similarity   77.8%;  Pred. No. 55;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              ||||||: |
Db         46 QRSGGSTQT 54


RESULT 5
US-09-071-035-212
; Sequence 212, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  212:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  60 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-212
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  Query Match             73.3%;  Score 33;  DB 4;  Length 60;
  Best Local Similarity   77.8%;  Pred. No. 55;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||| : |
Db         46 QRSGGSTQT 54


RESULT 6
US-09-071-035-206
; Sequence 206, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  206:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-206

  Query Match             73.3%;  Score 33;  DB 4;  Length 120;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||| : |
Db         70 QRSGGSTQT 78


RESULT 7
US-09-071-035-210
; Sequence 210, Application US/09071035
; Patent No. 6448043
;  GENERAL INFORMATION:
;    APPLICANT:  Gil H. Choi
;    TITLE OF INVENTION:  Enterococcus faecalis Polynucleotides and Polypeptides
;    NUMBER OF SEQUENCES:  496
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,035
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. Anders Brookes
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB369P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  210:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-035-210

  Query Match             73.3%;  Score 33;  DB 4;  Length 120;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||| : |
Db         70 QRSGGSTQT 78


RESULT 8
US-09-134-000C-6044
; Sequence 6044, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6044
;   LENGTH: 143
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-6044

  Query Match             73.3%;  Score 33;  DB 4;  Length 143;
  Best Local Similarity   77.8%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||| : |
Db         93 QRSGGSTQT 101


RESULT 9
US-09-489-039A-11488
; Sequence 11488, Application US/09489039A
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; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 11488
;   LENGTH: 407
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11488

  Query Match             73.3%;  Score 33;  DB 4;  Length 407;
  Best Local Similarity   75.0%;  Pred. No. 3.8e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSF 8
              || ||:||
Db         46 QRKGGNSF 53


RESULT 10
US-09-198-452A-579
; Sequence 579, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 579
;   LENGTH: 609
;   TYPE: PRT
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 1...609
;   OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-579

  Query Match             73.3%;  Score 33;  DB 4;  Length 609;
  Best Local Similarity   55.6%;  Pred. No. 5.7e+02;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |:|||:::|
Db        251 QKSGGAAYT 259


RESULT 11
US-09-543-681A-7112
; Sequence 7112, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7112
;   LENGTH: 1025
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-7112

  Query Match             73.3%;  Score 33;  DB 4;  Length 1025;
  Best Local Similarity   77.8%;  Pred. No. 9.6e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |  ||||||
Db         82 QWKGGSSFT 90


RESULT 12
US-08-026-138E-3
; Sequence 3, Application US/08026138E
; Patent No. 5502166
;  GENERAL INFORMATION:
;    APPLICANT:  Masayoshi MISHINA
;    TITLE OF INVENTION:  NOVEL PROTEINS AND GENES CODING THE SAME
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nishiohata Residence 1-107
;      STREET:  5214, Nishiohata-machi
;      CITY:  Niigata-shi
;      STATE:  Niigata-ken
;      COUNTRY:  JAPAN
;      ZIP:  951
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS v.5
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/026,138E
;      FILING DATE:  26-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 39563/1992
;      FILING DATE:  26-FEB-1992
;      APPLICATION NUMBER:  JP 173155/1992
;      FILING DATE:  30-JUN-1992
;      APPLICATION NUMBER:  JP 215017/1992
;      FILING DATE:  12-AUG-1992
;      APPLICATION NUMBER:  JP 303878/1992
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamburg, C.Bruce
;      REGISTRATION NUMBER:  22,389
;      REFERENCE/DOCKET NUMBER:  F-4551
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 986-2340
;      TELEFAX:  (212) 953-7733
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single strand
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  mouse
;      TISSUE TYPE:  brain
;    PUBLICATION INFORMATION:
;      AUTHORS:  Masayoshi MISHINA
;      TITLE:  NOVEL PROTEINS AND GENES CODING THE SAME
;      RELEVANT RESIDUES IN SEQ ID NO:  3: FROM 1 to 1239
US-08-026-138E-3

  Query Match             73.3%;  Score 33;  DB 1;  Length 1239;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 QRSGGSSFT 9
              ::||| |||
Db        590 KKSGGPSFT 598


RESULT 13
US-08-026-138E-4
; Sequence 4, Application US/08026138E
; Patent No. 5502166
;  GENERAL INFORMATION:
;    APPLICANT:  Masayoshi MISHINA
;    TITLE OF INVENTION:  NOVEL PROTEINS AND GENES CODING THE SAME
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nishiohata Residence 1-107
;      STREET:  5214, Nishiohata-machi
;      CITY:  Niigata-shi
;      STATE:  Niigata-ken
;      COUNTRY:  JAPAN
;      ZIP:  951
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS v.5
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/026,138E
;      FILING DATE:  26-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 39563/1992
;      FILING DATE:  26-FEB-1992
;      APPLICATION NUMBER:  JP 173155/1992
;      FILING DATE:  30-JUN-1992
;      APPLICATION NUMBER:  JP 215017/1992
;      FILING DATE:  12-AUG-1992
;      APPLICATION NUMBER:  JP 303878/1992
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamburg, C.Bruce
;      REGISTRATION NUMBER:  22,389
;      REFERENCE/DOCKET NUMBER:  F-4551
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 986-2340
;      TELEFAX:  (212) 953-7733
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1323 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single strand
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  mouse
;      TISSUE TYPE:  brain
;    PUBLICATION INFORMATION:
;      AUTHORS:  Masayoshi MISHINA
;      TITLE:  NOVEL PROTEINS AND GENES CODING THE SAME
;      RELEVANT RESIDUES IN SEQ ID NO:  4: FROM 1 to 1323
US-08-026-138E-4

  Query Match             73.3%;  Score 33;  DB 1;  Length 1323;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
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Db        617 KRPGGSTFT 625


RESULT 14
US-08-231-193A-58
; Sequence 58, Application US/08231193A
; Patent No. 5849895
;  GENERAL INFORMATION:
;    APPLICANT:  Daggett, Lorrie P.
;    APPLICANT:  Ellis, Steven B.
;    APPLICANT:  Liaw, Chen W.
;    APPLICANT:  Lu, Chin-Chun
;    TITLE OF INVENTION:  HUMAN N-METHYL-D-ASPARTATE RECEPTOR
;    TITLE OF INVENTION:  SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/231,193A
;      FILING DATE:  20-APR-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/052,459
;      FILING DATE:  20-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-9383
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-238-0999
;      TELEFAX:  619-238-0062
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-231-193A-58

  Query Match             73.3%;  Score 33;  DB 2;  Length 1336;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              :| |||:||
Db        620 KRPGGSTFT 628


RESULT 15
US-08-486-273A-58
; Sequence 58, Application US/08486273A
; Patent No. 5985586
;  GENERAL INFORMATION:
;    APPLICANT:  Daggett, Lorrie P.
;    APPLICANT:  Ellis, Steven B.
;    APPLICANT:  Liaw, Chen W.
;    APPLICANT:  Lu, Chin-Chun
;    TITLE OF INVENTION:  HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
;    TITLE OF INVENTION:  ENCODING SAME AND USES THEREFOR
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/486,273A
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/231,193
;       FILING DATE:  20-APR-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  6362-9383B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-238-0999
;       TELEFAX:  619-238-0062
;   INFORMATION FOR SEQ ID NO:  58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1336 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-486-273A-58

  Query Match             73.3%;  Score 33;  DB 2;  Length 1336;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              :| |||:||
Db        620 KRPGGSTFT 628


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 06:18:33 ; Search time 17.0459 Seconds
(without alignments)
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Title: US-10-684-957-43
Perfect score: 45
Sequence: 1 QRSGGSSFT 9

Scoring table: BLOSUM62
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Searched: 1759131 seqs, 391586102 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	17	US-10-684-957-43	Sequence 43, Appl
2	45	100.0	108	17	US-10-684-957-8	Sequence 8, Appli
3	45	100.0	108	17	US-10-684-957-12	Sequence 12, Appl
4	45	100.0	108	17	US-10-684-957-16	Sequence 16, Appl
5	45	100.0	215	17	US-10-684-957-18	Sequence 18, Appl
6	45	100.0	215	17	US-10-684-957-20	Sequence 20, Appl
7	45	100.0	215	17	US-10-684-957-22	Sequence 22, Appl
8	38	84.4	156	16	US-10-437-963-151445	Sequence 151445,
9	37	82.2	81	15	US-10-424-599-278251	Sequence 278251,
10	36	80.0	625	14	US-10-156-761-9381	Sequence 9381, Ap
11	35	77.8	107	11	US-09-864-408A-5386	Sequence 5386, Ap
12	35	77.8	117	16	US-10-425-115-318565	Sequence 318565,
13	35	77.8	126	16	US-10-767-701-52902	Sequence 52902, A
14	35	77.8	138	16	US-10-437-963-182245	Sequence 182245,
15	35	77.8	279	16	US-10-425-115-250950	Sequence 250950,
16	35	77.8	544	16	US-10-437-963-139896	Sequence 139896,
17	35	77.8	616	16	US-10-437-963-139897	Sequence 139897,
18	35	77.8	808	16	US-10-437-963-182374	Sequence 182374,
19	35	77.8	999	16	US-10-437-963-181440	Sequence 181440,
20	35	77.8	1055	16	US-10-437-963-183077	Sequence 183077,
21	34	75.6	148	17	US-10-732-923-18106	Sequence 18106, A
22	34	75.6	172	16	US-10-767-701-33919	Sequence 33919, A
23	34	75.6	215	16	US-10-425-115-330305	Sequence 330305,
24	34	75.6	302	9	US-09-874-923-122	Sequence 122, App
25	34	75.6	302	9	US-09-991-496-122	Sequence 122, App
26	34	75.6	384	15	US-10-424-599-155702	Sequence 155702,
27	34	75.6	696	16	US-10-425-115-297960	Sequence 297960,
28	34	75.6	709	9	US-09-874-923-121	Sequence 121, App
29	34	75.6	709	9	US-09-991-496-121	Sequence 121, App
30	34	75.6	752	16	US-10-425-115-279529	Sequence 279529,
31	34	75.6	846	16	US-10-425-115-279485	Sequence 279485,
32	34	75.6	1375	16	US-10-425-115-279507	Sequence 279507,
33	33	73.3	51	15	US-10-424-599-243091	Sequence 243091,
34	33	73.3	60	9	US-09-071-035-208	Sequence 208, App
35	33	73.3	60	9	US-09-071-035-212	Sequence 212, App
36	33	73.3	60	14	US-10-206-576-208	Sequence 208, App
37	33	73.3	60	14	US-10-206-576-212	Sequence 212, App
38	33	73.3	60	17	US-10-912-362-208	Sequence 208, App
39	33	73.3	60	17	US-10-912-362-212	Sequence 212, App
40	33	73.3	64	16	US-10-767-701-53161	Sequence 53161, A
41	33	73.3	120	9	US-09-071-035-206	Sequence 206, App
42	33	73.3	120	9	US-09-071-035-210	Sequence 210, App
43	33	73.3	120	14	US-10-206-576-206	Sequence 206, App
44	33	73.3	120	14	US-10-206-576-210	Sequence 210, App
45	33	73.3	120	17	US-10-912-362-206	Sequence 206, App

ALIGNMENTS

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RESULT 1
US-10-684-957-43
; Sequence 43, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-43

  Query Match            100.0%;  Score 45;  DB 17;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
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Db          1 QRSGGSSFT 9
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RESULT 2
US-10-684-957-8
; Sequence 8, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-8

Query Match 100.0%; Score 45; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
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Db 90 QRSGGSSFT 98

RESULT 3
US-10-684-957-12
; Sequence 12, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-12

Query Match 100.0%; Score 45; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 4
US-10-684-957-16
; Sequence 16, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-16

Query Match 100.0%; Score 45; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

RESULT 5
US-10-684-957-18
; Sequence 18, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm
; TITLE OF INVENTION: Pathway Inhibitors
; FILE REFERENCE: 01-1635-B
; CURRENT APPLICATION NUMBER: US/10/684,957
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-957-18

Query Match 100.0%; Score 45; DB 17; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRSGGSSFT 9
|||||||||
Db 90 QRSGGSSFT 98

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RESULT 6
US-10-684-957-20
; Sequence 20, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-20

  Query Match             100.0%;  Score 45;  DB 17;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||||||
Db         90 QRSGGSSFT 98


RESULT 7
US-10-684-957-22
; Sequence 22, Application US/10684957
; Publication No. US20050004353A1
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  APPLICANT:  Welcher, Andrew
;  APPLICANT:  Chute, Hilary
;  APPLICANT:  Li, Luke
;  APPLICANT:  Huang, Haichun
;  TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gam
;  TITLE OF INVENTION:  Pathway Inhibitors
;  FILE REFERENCE: 01-1635-B
;  CURRENT APPLICATION NUMBER: US/10/684,957
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/419,057
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/479,241
;  PRIOR FILING DATE: 2003-06-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-684-957-22

  Query Match             100.0%;  Score 45;  DB 17;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |||||||||
Db         90 QRSGGSSFT 98


RESULT 8
US-10-437-963-151445
; Sequence 151445, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151445
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_51588C.1.pep
US-10-437-963-151445

  Query Match             84.4%;  Score 38;  DB 16;  Length 156;
  Best Local Similarity   77.8%;  Pred. No. 48;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              ::|||||||
Db         30 RKSGGSSFT 38


RESULT 9
US-10-424-599-278251
; Sequence 278251, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278251
;   LENGTH: 81
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_93284C.1.pep
US-10-424-599-278251

  Query Match             82.2%;  Score 37;  DB 15;  Length 81;
  Best Local Similarity   77.8%;  Pred. No. 38;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              :|||||||:
Db         63 RRSGGSSFS 71


RESULT 10
US-10-156-761-9381
; Sequence 9381, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
```

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;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9381
;   LENGTH: 625
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis
US-10-156-761-9381

  Query Match             80.0%;  Score 36;  DB 14;  Length 625;
  Best Local Similarity   87.5%;  Pred. No. 4.4e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 RSGGSSFT 9
              | ||||||
Db        288 RDGGSSFT 295


RESULT 11
US-09-864-408A-5386
; Sequence 5386, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin D.
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Enco
;  FILE REFERENCE: 21402-012
;  CURRENT APPLICATION NUMBER: US/09/864,408A
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: 60/206,690
;  PRIOR FILING DATE: 2000-05-24
;  NUMBER OF SEQ ID NOS: 9068
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5386
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (41)..(41)
;   OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
US-09-864-408A-5386

  Query Match             77.8%;  Score 35;  DB 11;  Length 107;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QRSGGSSFT 9
              |:|||::||
Db         51 QQSGGTAFT 59


RESULT 12
US-10-425-115-318565
; Sequence 318565, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 318565
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_53605C.1.pep
US-10-425-115-318565

  Query Match             77.8%;  Score 35;  DB 16;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RSGGSSF 8
              |||||||
Db         60 RSGGSSF 66


RESULT 13
US-10-767-701-52902
; Sequence 52902, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 52902
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 13152599.pep
US-10-767-701-52902

  Query Match             77.8%;  Score 35;  DB 16;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RSGGSSF 8
              |||||||
Db         69 RSGGSSF 75


RESULT 14
US-10-437-963-182245
; Sequence 182245, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
```

; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182245
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(138)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79450C.1.pep
US-10-437-963-182245

Query Match 77.8%; Score 35; DB 16; Length 138;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 QRSGGSSFT 9
              ||||| | |
Db         14 QRSGGESLT 22
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RESULT 15
US-10-425-115-250950
; Sequence 250950, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 250950
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(279)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160454C.1.pep
US-10-425-115-250950

Query Match 77.8%; Score 35; DB 16; Length 279;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 RSGGSSF 8
              |||||||
Db         69 RSGGSSF 75
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Search completed: August 18, 2005, 07:08:04
Job time : 17.1709 secs

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